

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 8, 2005, 01:28:17 ; Search time 3431 Seconds
(without alignments)
6202.508 Million cell updates/sec

Title: US-10-663-157-3

Perfect score: 584

Sequence: 1 ggcgcgcgmngngcaag.....agaattacctgtgtgcc 584

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hic:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gss1:*

9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	515.2	88.2	836	4	BI465085
2	512	87.7	975	5	BQ927810
3	498.6	85.4	882	5	BQ688267
4	486	83.2	526	2	BF433925
5	481.8	82.5	875	4	BI544644
6	474.8	81.3	743	4	BG773091
7	440.8	75.5	482	2	BF512756
8	417.2	71.4	1118	2	BE615766
9	413.6	70.8	452	7	N49208
10	398	68.2	503	2	BE049432
11	385	65.9	913	5	BQ887029
12	385	65.9	3628	3	AK043823
13	384.6	65.9	645	6	CA333708
14	382.6	65.5	420	1	AA918818
15	372	63.7	497	1	AL138519
16	368.2	63.0	3597	3	AK033529
17	366	62.7	824	2	BE867582
18	364.6	62.4	600	6	CA528743
19	355.6	60.9	829	4	BI649863
20	349.8	59.9	732	1	AI663485
21	349	59.8	959	2	BE563227
22	348.2	59.6	822	4	BI649277
23	335.2	57.4	1039	7	CF593305
24	323	55.3	521	2	AW263837

25	315.8	54.1	953	6	CA976916	CA976916	AGENCOURT
26	306.8	52.5	766	4	BG752486	BG752486	AGENCOURT
27	291.8	50.0	528	1	AU129537	AU129537	AGENCOURT
28	291.2	49.9	849	2	BF687212	BF687212	AGENCOURT
29	289.8	49.6	593	4	BI544954	BI544954	AGENCOURT
30	283	48.5	950	5	BQ950513	BQ950513	AGENCOURT
31	279.8	47.9	486	7	CN373267	CN373267	AGENCOURT
32	279	47.8	759	4	BI561782	BI561782	AGENCOURT
33	270	46.2	912	2	BF530378	BF530378	AGENCOURT
34	264.8	45.3	473	7	CN373269	CN373269	AGENCOURT
35	262.8	45.0	825	4	BI110344	BI110344	AGENCOURT
36	253	43.3	651	6	BY731428	BY731428	AGENCOURT
37	238.4	40.8	637	2	BB624973	BB624973	AGENCOURT
38	237.4	40.7	638	6	BY718537	BY718537	AGENCOURT
39	223	38.2	744	5	BU599647	BU599647	AGENCOURT
40	221.2	37.9	513	5	BO555510	BO555510	AGENCOURT
41	218.8	37.5	678	9	CG503364	CG503364	AGENCOURT
42	218.6	37.4	373	9	CE182320	CE182320	AGENCOURT
43	212	36.3	537	7	CN298860	CN298860	AGENCOURT
44	210.8	36.1	876	5	BX389844	BX389844	AGENCOURT
45	208.8	35.8	405	7	CN373259	CN373259	AGENCOURT

ALIGNMENTS

RESULT 1

BI465085

LOCUS

DEFINITION

603206493F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5272054 5',

mRNA sequence.

ACCESSION

BI465085

VERSION

BI465085.1

KEYWORDS

EST.

SOURCE

ORGANISM

Homo sapiens (human)

REFERENCE

1 (bases 1 to 836)

NIH-MGC http://mgc.ncl.nih.gov/.

AUTHORS

National Institutes of Health,

Unpublished (1999)

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgaabs-r@mail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki

Toshiyuki and Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM11686 row: j column: 23

High quality sequence stop: 791.

Location/Qualifiers

1. .836

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5272054"

/lab_host="DH10B"

/clone_lib="NIH_MGC_97"

/note="Organ: testis; Vector: pBluescriptR (modified

pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI

(gucgag); Oligo-dT primed using primer

5'-TTTTTTTTTTTTTN-3', size-selected for average

insert size 2.2 kb and normalized to ROT 5. This is a

primary library enriched for full-length clones and

constructed using the Cap-trapper method (Carninci, in

preparation). Library constructed by M. Brownstein

(NIH/NHGRI, National Institutes of Health). Note: this is

a NIH_MGC Library."

ORIGIN

Query Match 88.2%; Score 515.2; DB 4; Length 836;
Best Local Similarity 94.7%; Pred. No. 8.7e-116;
Matches 551; Conservative 0; Mismatches 29; Indels 2; Gaps 2;

QY 1 GCGNCCGCGNNGNGCAAGTGTCTGAGCGCCCTAGNGCCTCCCTTGGCGCTCCCTCC 60
DB 189 GCGCGCGCGCTGGCAGGTCTGAGCGCCCTAGAGCTCCCTTGGCGCTCCCTCC 248
QY 61 TCTGCCCGCGCTAGCAGTGCATGATGGGTGTGGAGGTAGATGGGTCCCGG-CCGGGA 119
DB 249 TCTGCCCGCGCGCAGCAGTGCATGATGGGTGTGGAGGTAGATGGGTCCCGGCGCGGA 308
QY 120 GCGCGCGGTGGATGCGCGCTGGGAGAGCAGCCCGCATTCACGTCCCGCGCGCC 179
DB 309 GCGCGCGGTGGATGCGCGCTGGGAGAGCAGCCCGCATTCACGTCCCGCGCGCC 368
QY 180 CC-GGGCACCTTCGAGTCCCGGTTCAGCATCGGGGACCTCTCCGAGCAGCAGCCGC 238
DB 369 CCGGGCGCCCTGGAGTCCCGGTTCAGCATCGGGGACCTCTCCGAGCAGCAGCCGC 428
QY 239 CTTGCCCTCTGAGCGGCATTCGCGCGCGAGCCAGCCAGCCAGTATGATGCGGGTCCCT 298
DB 429 CTTGCCCTCTGAGCGGCATTCGCGCGCGAGCCAGCCAGCCAGTATGATGCGGGTCCCT 488
QY 299 TCTCCTGCTTGGATTCCTTAGCACCACACAGCTCAGCCAGACAGAGCCCTCGAATCT 358
DB 489 TCTCCTGCTTGGATTCCTTAGCACCACACAGCTCAGCCAGACAGAGCCCTCGAATCT 548
QY 359 CATTTGGCACATACCGGCATTTGACCGTGCCACCGCGCGAGTGTCTAACCTGTGACAAGTG 418
DB 549 CATTTGGCACATACCGGCATTTGACCGTGCCACCGCGCGAGTGTCTAACCTGTGACAAGTG 608
QY 419 TCAGCAGGAACTATGTCTCTGAGCATTTGTACACAGCAAGCTCGCGGTCTGCAAGCAG 478
DB 609 TCAGCAGGAACTATGTCTCTGAGCATTTGTACACACAGCAAGCTCGCGGTCTGCAAGCAG 668
QY 479 TTCGCCCTGTGGGACCTTTACAGGCGATGAGATGGCATAGAGAAATGCCATGCTGTAG 538
DB 669 TGGCCTGTGGGACCTTTACAGGCGATGAGATGGCATAGAGAAATGCCATGCTGTAG 728
QY 539 TCAGCCATGCCCATGGCCAAATGATTGAGAAATTAACCTTTGTGC 580
DB 729 TCAGCAATGCCCATGGCCAAATGATTGAGAAATTAACCTTTGTGC 770

RESULT 2
BQ927810
LOCUS
DEFINITION BQ927810 975 bp mRNA linear EST 20-AUG-2002
AGENCOURT 8822280 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:6381568
5', mRNA sequence.

ACCESSION BQ927810
VERSION BQ927810.1 GI:22342841
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLCM2571 row: p column: 17
High quality sequence stop: 498.

FEATURES

Location/Qualifiers
1. 975
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6381568"
/tissue_type="carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_40"
/note="Organ: prostate; Vector: pOTB7; Site: 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN

Query Match 87.7%; Score 512; DB 5; Length 975;
Best Local Similarity 95.1%; Pred. No. 5.4e-115;
Matches 557; Conservative 0; Mismatches 26; Indels 3; Gaps 3;

QY 1 GCGNCCGCGNNGNGCAAGTGTCTGAGCGCCCTAGNGCCTCCCTTGGCGCTCCCTCC 60
DB 151 GCGCGCGCGCTGGCAGGTCTGAGCGCCCTAGAGCCTCCCTTGGCGCTCCCTCC 210
QY 61 TCTGCCCGCGCTAGCAGTGCATGAGGTGTGGAGGTAGATGGGTCCCGG-CCGGGA 119
DB 211 TCTGCCCGCGCGCAGCAGTGCATGAGGTGTGGAGGTAGATGGGTCCCGGCGCGGA 270
QY 120 GCGCGCGGTGGATGCGCGCTGGGAGAGCAGCGCGATTCACAGCTGCCCCGCGCGC 179
DB 271 GCGCGCGGTGGATGCGCGCTGGGAGAGCAGCGCGATTCACAGCTGCCCCGCGCGC 330
QY 180 CC-GGGCACCTTTGCGAGTCCCGGTTCAGCCATGGGGACCTCTCCGAGCAGCAGCCGC 238
DB 331 CCGGGCGCCCTGCGAGTCCCGGTTCAGCCATGGGGACCTCTCCGAGCAGCAGCCGC 390
QY 239 CTTGCCCTCTGAGCGGCATTCGCGCGAGCCAGCCAGCAGTATGCGGGTCCCT 298
DB 391 CTTGCCCTCTGAGCGGCATTCGCGCGAGCCAGCCAGCAGTATGCGGGTCCCT 450
QY 299 TCTCCTGCTTGGATTCCTTAGCACCACACAGCTCAGCCAGAAAGAGGCCCTCGAATCT 358
DB 451 TCTCCTGCTTGGATTCCTTAGCACCACACAGCTCAGCCAGAAAGAGGCCCTCGAATCT 510
QY 359 CATTTGGCACATACCGGCATTTGACCGTGCCACCGCGCGAGTGTCTAACCTGTGACAAGTG 418
DB 511 CATTTGGCACATACCGGCATTTGACCGTGCCACCGCGCGAGTGTCTAACCTGTGACAAGTG 570
QY 419 TCAGCAGGAACTATGTCTCTGAGCATTTGACCAACACAGCCCTGCGGTCTGCAGCAG 478
DB 571 TCAGCAGGAACTATGTCTCTGAGCATTTGTA-CAACACACCGCTGCGGTCTGCAGCAG 629
QY 479 TTTGCCCTGTGGGACCTTTTACAGGCATGAGATGGCATAGAGAAATGCCATGCTGTAG 538
DB 630 TTTGCCCTGTGGGACCTTTTACAGGCATGAGATGGCATAGAGAAATGCCATGCTGTAG 689
QY 539 TCAGCCATGCCCATGGCCAAATGATTGAGAAATTAACCTTTGTGTGC 584
DB 690 TCAGCCATGCCCATGGCCAAATGATTGAGAAATTAACCTTTGTGTGC 735

RESULT 3
BQ688267
LOCUS
DEFINITION BQ688267 882 bp mRNA linear EST 15-JUL-2002
AGENCOURT 8047240 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6207591
5', mRNA sequence.

ACCESSION BQ688267
VERSION BQ688267.1 GI:21813583
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 882)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Note: L1CM2363 row: 0 column: 16
High quality sequence stop: 689.
FEATURES
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Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
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/lab_host="DH10B (phage-resistant)"
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/notes="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; CDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN

Query Match 85.4%; Score 498.6; DB 5; Length 882;
Best Local Similarity 98.9%; Pred. No. 1e-111;
Matches 523; Conservative 0; Mismatches 4; Indels 2; Gaps 2;
Qy 58 TCCTCTCCCGCGCGTTCAGTGTGATGCGGTGTTGGAGGTAGATGGGTCTCCGG-CCG 116
Db 1 TCCTCTCCCGCGCGCGTTCAGTGTGATGCGGTGTTGGAGGTAGATGGGTCTCCGGCGCG 60
Qy 117 GGAGCGCGCGTTCAGTGTGATGCGGTGTTGGAGGTAGATGGGTCTCCGGCGCG 176
Db 61 GGAGCGCGCGTTCAGTGTGATGCGGTGTTGGAGGTAGATGGGTCTCCGGCGCG 120
Qy 177 GCGCC- GCGCCACCTTCGAGTTCGCCGTTTCAGCCATGGGACCTCTCCGAGCAGCAGCAC 235
Db 121 GCGCCGCGCGCGTTCAGTGTGATGCGGTGTTGGAGGTAGATGGGTCTCCGGCGCG 180
Qy 236 CGCGCTCGCTTCGAGCGCGATTCGCCCGCGAGCCACAGCCACGATGATCGCGGCTC 295
Db 181 CGCGCTCGCTTCGAGCGCGATTCGCCCGCGAGCCACAGCCACGATGATCGCGGCTC 240
Qy 296 CTTCTCTCTGTTGGATTCTTAGCACCACAGCTCAGCCAGCAGCAGAGCGCTCGAA 355
Db 241 CTTCTCTCTGTTGGATTCTTAGCACCACAGCTCAGCCAGCAGCAGAGCGCTCGAA 300
Qy 356 TCTCATTTGGCAGATACCGCCATGTTGACCGTCCCGCGAGCGCGAGTGCTAACCTGTGACAA 415
Db 301 TCTCATTTGGCAGATACCGCCATGTTGACCGTCCCGAGCGCGAGTGCTAACCTGTGACAA 360
Qy 416 GTGTCCAGCAGGAACCTATGCTCTGAGCATTTGTACCAACAGCCTCGCGCTCTCGAG 475
Db 361 GTGTCCAGCAGGAACCTATGCTCTGAGCATTTGTACCAACAGCCTCGCGCTCTCGAG 420
Qy 476 CAGTTGCGCTGTGGGGACCTTTACCGGCATGAGATGGCATAGAGAAATGCCATGACTG 535
Db 421 CAGTTGCGCTGTGGGGACCTTTACCGGCATGAGATGGCATAGAGAAATGCCATGACTG 480

Qy 536 TAGTCAGCCATGCCCATGCCAATGATTGAGAAATACCTTGTGTGCTGCC 584
Db 481 TAGTCAGCCATGCCCATGCCAATGATTGAGAAATACCTTGTGTGCTGCC 529
RESULT 4
BF433925 526 bp mRNA linear EST 30-MAR-2001
LOCUS 7q56g07.x1 NCI CGAP Lu24 Homo sapiens CDNA clone IMAGE:3702349 3,
DEFINITION similar to TR:O75505 O75509 TNFR-RELATED DEATH RECEPTOR-6,
; contains MER22.t2 PTR5 repetitive element ; mRNA sequence.
ACCESSION BF433925
VERSION 1 (bases 1 to 526)
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 526)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 427.
FEATURES
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/db_xref="taxon:9606"
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/notes="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Plasmid DNA from the normalized
library NCI CGAP Lu5 was prepared, and as circles were
made in vitro. Following HAP purification, this DNA was
used as tracer in a subtractive hybridization reaction.
The driver was PCR-amplified cDNAs from a pool of 5,000
clones made from the same library (cloneIDs
1414920-1417991 and 1520904-1522439). Subtraction by Bento
Soares and M. Fatima Bonaudo."

Query Match 83.2%; Score 486; DB 2; Length 526;
Best Local Similarity 97.7%; Pred. No. 1.2e-108;
Matches 514; Conservative 0; Mismatches 10; Indels 2; Gaps 2;
Qy 52 CTTCTCTCTCTCTCCCGCGCGTTCAGTGTGATGCGGTGTTGGAGGTAGATGGGTCCC 111
Db 1 CTTCTCTCTCTCTCCCGCGCGCGTTCAGTGTGATGCGGTGTTGGAGGTAGATGGGTCCC 60
Qy 112 GG-CCGCGAGCGCGCGTTCAGTGTGATGCGGTGTTGGAGGTAGATGGGTCCC 170
Db 61 GGCGCGGAGCGCGCGTTCAGTGTGATGCGGTGTTGGAGGTAGATGGGTCCC 120
Qy 171 CCGCGCGCGCGCG- GCGCACCTTTCAGTGTCCCGCGTTCAGCCATGGGACCTCTCCGAGCAG 229
Db 121 CCGCGCGCGCGCGCGCGCTTCAGTGTCCCGCGTTCAGCCATGGGACCTCTCCGAGCAG 180
Qy 230 CAGCACCGCGCTCTCGCTCTCTGCGCGCGATCGCCCGCGCGACCCACGACGATGATCGC 289

Db 181 CAGCACCAGCCCTCGCCTCTGACGCGCATGGCCCGCGAGCCACAGCCACGATGATGC 240
 QY 290 GGGCTCCCTTCCTCTGATTCCTAGCAGCCACACAGCTCAGCCAGACAGAGGC 349
 Db 241 GGGCTCCCTTCCTCTGATTCCTAGCAGCCACACAGCTCAGCCAGACAGAGGC 300
 QY 350 CTCGAATCTCATTGGCAGCATACCGCCATGTTGACCGTGGCCCGGCGAGGTCTAACCTG 409
 Db 301 CTCGAATCTCATTGGCAGCATACCGCCATGTTGACCGTGGCCCGGCGAGGTCTAACCTG 360
 QY 410 TGCAAGTGTCCAGCAGGAACTATGTTCTGAGCATTTGACCAACAGGCTGCGCT 469
 Db 361 TGCAAGTGTCCAGCAGGAACTATGTTCTGAGCATTTGACCAACAGGCTGCGCT 420
 QY 470 CTCGACAGTGGCCCTGTGGGACCTTTACCGAGCATGAGATGGCATAGAGAAATGCCA 529
 Db 421 CTCGACAGTGGCCCTGTGGGACCTTTACCGAGCATGAGATGGCATAGAGAAATGCCA 480
 QY 530 TGAATCTAGTACGATGCGCCATGGCCATGATTGAGAAATTAACCT 575
 Db 481 TGAATCTAGTACGATGCGCCATGGCCATGATTGAGAAATTAACCT 526

RESULT 5
 BI544644
 LOCUS 603242292F1 NIH_MGC_95 875 bp mRNA linear EST 05-SEP-2001
 DEFINITION mRNA sequence.
 ACCESSION BI544644
 VERSION BI544644.1 GI:15431956
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 875)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
 Toshiyuki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM11719 row: h column: 24
 High quality sequence stop: 785.
 Location/Qualifiers
 1..875
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5284679"
 /tissue_type="hippocampus"
 /lab_host="DH10B"
 /notes="Organ: brain; Vector: pBluescriptR (modified
 pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI
 (GTCGAG); Oligo-dT primed using primer
 5'-TTTTTTTTTTTTTTVN-3', size-selected for average
 insert size 2.5 kb and normalized to 10^5. This is a
 primary library enriched for full-length clones and
 constructed using the Cap-trapper method (Carninci, in
 preparation). Library constructed by M. Brownstein
 (NIH/NHGRI, National Institutes of Health). Note: this
 is a NIH_MGC Library."

FEATURES
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 /organism="Homo sapiens"
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 pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI
 (GTCGAG); Oligo-dT primed using primer
 5'-TTTTTTTTTTTTTTVN-3', size-selected for average
 insert size 2.5 kb and normalized to 10^5. This is a
 primary library enriched for full-length clones and
 constructed using the Cap-trapper method (Carninci, in
 preparation). Library constructed by M. Brownstein
 (NIH/NHGRI, National Institutes of Health). Note: this
 is a NIH_MGC Library."

Query Match 82.5%; Score 481.8; DB 4; Length 875;
 ORIGIN

Best Local Similarity 95.1%; Pred. No. 1.4e-107;
 Matches 558; Conservative 0; Mismatches 23; Indels 6; Gaps 6;
 QY 1 GGCNCCGNNNGNGCAAGTGTGACGCGCCCTAGNGCCTCCCTTCCGCGCTCCCTCC 60
 Db 220 GCGCGCGCGCGCTGGGCGAGGTGTGAGCGCCCTAGAGCTCCCTTCCGCGCTCCCTCC 279
 QY 61 TCTGCGCGCGCGCTAGCAGTGCACATGGGCTGTGGAGGTAGATGGCTCCCGG-CGGGA 119
 Db 280 TCTGCGCGCGCGCGCAGTGCACATGGGCTGTGGAGGTAGATGGCTCCCGGCGCGGA 339
 QY 120 GCGCGCGGTGAGTGGCGCTGGGAGAGCAGCGCGCATTCAGCTTCCAGCTGCCCGCGCGC 179
 Db 340 GCGCGCGGTGAGTGGCGCTGGGAGAGCAGCGCGCATTCAGCTGCCCGCGCGC 399
 QY 180 CC-GGCGACCTTGGAGTCCCGGTTAGCCATGGGACCTCTCGAGCAGCAGCAGCCG 238
 Db 400 CGGCGCGCGCTGGAGTCCCGGTTAGCCATGGGACCTCTCGAGCAGCAGCAGCCAC 459
 QY 239 CCTCGCCTCTCGAGCGCATCGCCCGCGAGCCACAGCAGATGATCGCGGCTCCCT 298
 Db 460 CCTCGCCTCTCGAGCGCATCGCCCGCGAGCCACAGCAGATGATCGCGGCTCCCT 519
 QY 299 TCTCTGCTGGATTCCTTAGCACACACAGCTCAGCCAGAACAGAA-GGCTCGAATC 357
 Db 520 TCTCTGCTGGATTCCTTAGCACACACAGCTCAGCCAGAACAGAAAGGCGCTCGAATC 579
 QY 358 TCATTTGGCAC-ATACCGCATGTTACCGTCCCGCGAGCGCGCTTACCTGTGCAAG 416
 Db 580 TCATTTGGCACATACCGCATGTTACCGTCCCGCGAGCGCGCTTACCTGTGCAAG 639
 QY 417 TGTCCAGCAGGAACCTATGCTCTGAGCATTTGACAAACAGAGCTTGGCTCTGCAG- 475
 Db 640 TGTCCAGCAGGAACCTATGCTCTGAGCATTTGACAAACAGAGCTTGGCTCTGCAGC 699
 QY 476 CAGTTGCCCTTGGGAGCTTTACAGGATGAGAAATGCGATAGAGAAATGCCATG-ACT 534
 Db 700 CAGTTGCCCTTGGGAGCTTTACAGGATGAGAAATGCGATAGAGAAATGCCATG- 759
 QY 535 GTAGTCAGCCATGCCCATGGCAATGATTGAGAAATTAACCTTGTCT 581
 Db 760 GTAGTCAGCCATGCCCATGGCAATGATTGAGAAATTAACCTTGTCT 806
 RESULT 6
 BG773091 743 bp mRNA linear EST 15-MAY-2001
 LOCUS 602721804F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4838808 5',
 DEFINITION mRNA sequence.
 ACCESSION BG773091
 VERSION BG773091.1 GI:14083744
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 743)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
 Toshiyuki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM10773 row: g column: 01
 High quality sequence stop: 736.
 Location/Qualifiers

FEATURES

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source 1. 743
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4838808"
/lab_host="DH10B"
/clone_lib="NIH_MGC_97"
/notes="Organ: testis; Vector: pBluescriptR (modified
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI
(gtcgag); Oligo-dt primed using primer
5'-TTTTTTTTTTTTTWN-3', size-selected for average
insert size 2.2 kb and normalized to 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIMH/NHGRI, National Institutes of Health). Note: this is
a NIH_MGC Library."
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ORIGIN

Query Match 81.3%; Score 474.8; DB 4; Length 743;
Best Local Similarity 97.1%; Pred. No. 7.1e-106;
Matches 501; Conservative 0; Mismatches 13; Indels 2; Gaps 2;

QY 1 GCGNCCGCGNNGNGCAAGTGTGAGCGCCCTAGNGCCTCTTGGCGCTCCCTCCCTCC 60
| | | | |
Db 228 GCGGCGCGCGCGTGTGGCAGGTGTGAGCGCCCTAGAGCCTCTTGGCGCTCCCTCC 287
| | | | |
QY 61 TCTGCCCGCGGTAGCAGTGCACATGGGGTGTGGAGGTAGTGGTCCCGG-CCGGGA 119
| | | | |
Db 288 TCTGCCCGCGCGCAGCAGTGCACATGGGGTGTGGAGGTAGTGGTCCCGGCGCGGA 347
| | | | |
QY 120 GCGCGCGGTGGATGCGCGCTGGGCGAAGCAGCGCGCGATTCAGCTGCGCGCGCGCC 179
| | | | |
Db 348 GCGCGCGGTGGATGCGCGCTGGGCGAAGCAGCGCGCGATTCAGCTGCGCGCGCC 407
| | | | |
QY 180 CC-GGCCACCTTGGAGTCCCGGTTGAGCATGGGGACCTCTCCGAGCAGCAGCCGC 238
| | | | |
Db 408 CCGGGCGCGCTCGCATGCTCCCGGTTGAGCATGGGGACCTCTCCGAGCAGCAGCCGC 467
| | | | |
QY 239 CTTGCGCTCTCGAGCGCATGCGCGCGAGCCAGCCAGCATGATGCGGGCTCCCT 298
| | | | |
Db 468 CTTGCGCTCTCGAGCGCATGCGCGCGAGCCAGCCAGCATGATGCGGGCTCCCT 527
| | | | |
QY 299 TCTCTGCTTGGATTCCTTAGCACCACAGCTCAGCCAGCAGCAGAGGCTCGAATCT 358
| | | | |
Db 528 TCTCTGCTTGGATTCCTTAGCACCACAGCTCAGCCAGCAGCAGAGGCTCGAATCT 587
| | | | |
QY 359 CATTTGCACATACCGCATGTTGACCGTGCACCGCGCAGGTCTAACCTGTGACAAGTG 418
| | | | |
Db 588 CATTTGCACATACCGCATGTTGACCGTGCACCGCGCAGGTCTAACCTGTGACAAGTG 647
| | | | |
QY 419 TCCAGCAGGAACCTATGCTCTGAGCATTTGACCAACAGCAGCAGCTGCGGTCTGACGAG 478
| | | | |
Db 648 TCCAGCAGGAACCTATGCTCTGAGCATTTGACCAACAGCAGCAGCTGCGGTCTGACGAG 707
| | | | |
QY 479 TTGCGCTGTGGGACCTTTACCGAGCATGAGATGG 514
| | | | |
Db 708 TTGCGCTGTGGGACCTTTACCGAGCATGAGATGG 743
| | | | |

RESULT 7
BF512756
LOCUS
DEFINITION UI-H-BMI-amm-f-03-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone
IMAGE:3070588 3', mRNA sequence.
BF512756
ACCESSION
VERSION
KEYWORDS
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 482)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapsb@mail.nih.gov
Oligo-dt track not found, Not 1 site shown in beginning of sequence
is likely internal to the message. cDNA library preparation: M.B.
Soares Lab Clone distribution: NCI-CGAP clone distribution
Information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html The following repetitive
elements were found in this cDNA sequence: 188-190,
>GC rich#Low complexity
Seq primer: M13 Forward
POLYA=No.

Location/Qualifiers
1. 482
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3070588"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_Sub7"
/notes="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not 1; Site 2: Eco RI; NCI CGAP Sub7
is a subtracted library derived from NCI CGAP Sub6. The
NCI CGAP Sub7 library had 12 million recombinants. A
single-stranded DNA preparation of NCI_CGAP_Sub6 was used
as a tracer in a subtractive hybridization with a driver
comprising: the IMAGE pool (NCI CGAP Kid3 pool 1 LLAM
3334-3337, 3682-3683, 3798-3803 (IMAGE CloneIDb
1322376-1323911, 1456008-1456775, 1500552-1502855);
NCI CGAP Kid5 pool 1 LLAM 3338-3342, 3722-3725, 3776-3778
(IMAGE CloneIDb 1323912-1325831, 1471368-1472803,
1492104-1493255); NCI CGAP_Lus pool 1 LLAM 3575-3582,
3851-3854 (IMAGE CloneIDb 1414920-1417991,
1520904-1522439); NCI CGAP GC4 pool 1 LLAM 3164-3167,
3716-3720, 3733-3735 (IMAGE CloneIDb
1257096-1258631, 1469064-1470983, 1475592-1476743);
NCI CGAP_Pr22 pool 1 LLAM 2457-2459, 2758-2759, 3062-3068
(IMAGE CloneIDb 985608-986759, 1101192-1101959,
1217928-1220615); NCI CGAP_Co1 pool 1 LLAM 2644-2653,
2871-2872 (IMAGE CloneIDb
1057416-1061255, 1144584-1145351). (6% of the driver
population), plus a pool of 3,840 arrayed clones from
NCI CGAP_Sub1 (IMAGE CloneIDb 2708616-2710535) and
NCI CGAP_Sub2 (IMAGE CloneIDb 2710536-2712455) (4% of
the driver population), plus a pool of 11,136 clones from
NCI CGAP_Sub3 (IMAGE CloneIDb 2712456-2723591) (10% of
the driver population), plus a pool of 5,472 clones from
NCI CGAP_Sub4 (IMAGE CloneIDb 2723592-2729326) (40% of the
driver population), plus a pool of 4032 clones from
NCI CGAP_Sub6 (IMAGE CloneIDb 2728969-2733190) (40% of the
driver population). Subtraction was performed as
previously described [Bonaldo, Lennon & Soares (1996):
Normalization and Subtraction: Two Approaches To
Facilitate Gene Discovery. Genome Research 6, 791-806.
TAG_SEQ=None found"

Query Match 75.5%; Score 440.8; DB 2; Length 482;
Best Local Similarity 96.9%; Pred. No. 1.5e-97;
Matches 467; Conservative 0; Mismatches 13; Indels 2; Gaps 2;

QY 2 CGNCCGCGNNGNGCAAGTGTGAGCGCCCTAGNGCCTCTTGGCGCTCCCTCCCTCT 61
| | | | |
Db 1 CGGCGCGCGCGCTGGGCGAGTGTGAGCGCCCTAGAGCCTCTTGGCGCTCCCTCT 60
| | | | |
QY 62 CTGCCCCGCGGTAGCAGTGCACATGGGGTGTGGAGGTAGATGGCTCCCGG-CCGGGAG 120
| | | | |
Db 61 CTGCCCCGCGGACGAGTGCACATGGGGTGTGGAGGTAGATGGCTCCCGGCGCGGAG 120
| | | | |
QY 121 GCGGCGGTGGATGCGCGCGCTGGGCGAGCAGCGCGCGGATTCAGAGTGGCCCCCGCGCC 180
| | | | |

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Db      121  CGCGCGGTGGATGTCGCGCTGGGAGAGCAGCGCGCGATTCCAGCTGCCCCGGCGGCC 180
Qy      181  C-GGCCACCTTGGAGTCCCGGTTTCCAGCCATGGGAGACCTCCCGAGAGCAGCAGCGCC 239
Db      181  CGGCGCCCGCTCGAGTCCCGGTTTCCAGCCATGGGAGACCTCCCGAGAGCAGCAGCGCC 240
Qy      240  CTCGCTCTCTGACGCGCATCGCGCCGAGCCACAGCCAGCATGATCGCGGCTCCCTT 299
Db      241  CTCGCTCTCTGACGCGCATCGCGCCGAGCCACAGCCAGCATGATCGCGGCTCCCTT 300
Qy      300  CTCGCTCTCTGATTCCTTAGCACCCACAGCTCAGCCAGAGAGCCCTCGAATCTC 359
Db      301  CTCGCTCTCTGATTCCTTAGCACCCACAGCTCAGCCAGAGAGCCCTCGAATCTC 360
Qy      360  ATTGGACATACCGCATGTTGACCTGACCGTGCACCGCCAGGTGTAACCTGTGACAGTGT 419
Db      361  ATTGGACATACCGCATGTTGACCGTGCACCGCCAGGTGTAACCTGTGACAGTGT 420
Qy      420  CCAGCAGGAACCTATGCTCTGAGCATTTGACCAACAGAGCCCTGCGCTTGCAGCAGT 479
Db      421  CCAGCAGGAACCTATGCTCTGAGCATTTGACCAACAGAGCCCTGCGCTTGCAGCAGT 480
Qy      480  TG 481
Db      481  TG 482
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RESULT 8
BE615766
LOCUS   601279916F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3622107 5',
DEFINITION mRNA sequence.
ACCESSION BE615766
VERSION   BE615766.1 GI:9897365
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE     NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL   National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT   Unpublished (1999)
          Contact: Robert Strauberg, Ph.D.
          Email: csapbs-@email.nih.gov
          Tissue Procurement: ATCC
          CDNA Library Preparation: Ling Hong/Rubin Laboratory
          CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: LLCM296 row: o column: 04
          High quality sequence stop: 716.
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FEATURES
source    Location/Qualifiers
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            /clone="IMAGE:3622107"
            /tissue_type="adenocarcinoma"
            /lab_host="DH10B (phage-resistant)"
            /clone_lib="NIH_MGC_39"
            /notes="Organ: pancreas; Vector: pOTB7; Site1: XhoI;
            Site 2: EcoRI; cDNA made by oligo-dT priming.
            Directionally cloned into EcoRI/XhoI sites using the
            following 5' adaptor: GGCACGAG(G). Library constructed
            by Ling Hong in the laboratory of Gerald M. Rubin
            (University of California, Berkeley) using ZAP-cDNA
            synthesis kit (Stratagene) and Superscript II RT (Life
            Technologies)."
```

ORIGIN

```
Query Match 71.4%; Score 417.2; DB 2; Length 1118;
Best Local Similarity 98.7%; Pred No. 1e-91;
Matches 452; Conservative 0; Mismatches 3; Indels 3; Gaps 3;
Qy      130  GATCGGCGCTGGGAGAGCAGCGCGATTCCAGTTCAGCTGCCCCGGCGGCC 188
Db      130  GATCGGCGCTGGGAGAGCAGCGCGATTCCAGTTCAGCTGCCCCGGCGGCC 60
Qy      189  TTGCGAGTCCCGGTTTCCAGCCATGGGACCTCTCCGAGCAGCAGCAGCCCTCGCTCC 248
Db      61  TTGCGAGTCCCGGTTTCCAGCCATGGGACCTCTCCGAGCAGCAGCAGCCCTCGCTCC 120
Qy      249  TGCAGCCGATCGCGCGCGGACACAGCAGATGATCGCGGCTCCCTTCTCTCTGCTT 308
Db      121  TGCAGCCGATCGCGCGCGGACACAGCAGATGATCGCGGCTCCCTTCTCTCTGCTT 180
Qy      309  GGATTCCTTAGCACCCACAGCTCAGCCAGAGAGAGGCTCGAATCTCATTTGGCACA 368
Db      181  GGATTCCTTAGCACCCACAGCTCAGCCAGAGAGAGGCTCGAATCTCATTTGGCACA 240
Qy      369  TACCGCCATGTTGACCGTGCACCGCCAGGTGCTAACTGTGACAAGTTCACAGCA 428
Db      241  TACCGCCATGTTGACCGTGCACCGCCAGGTGCTAACTGTGACAAGTTCACAGCA 300
Qy      429  ACCTATGCTCTGAGCATTTGTACCAACAGCGCTCGCGCTCTGAGCAGATTTGCCCTGTG 488
Db      301  ACCTATGCTCTGAGCATTTGTACCAACAGCGCTCGCGCTCTGAGCAGATTTGCCCTGTG 360
Qy      489  GGGACCTTTACCGAGCATGA-GAATGGCATAGAG-AAATGGCATGCTGTAGTCAGCCAT 546
Db      361  GGGACCTTTACCGAGCATGAGCAATGGCATAGAGCAATGCCATGACTGTAGTCAGCCAT 420
Qy      547  GCCCATGGCCATGATTGAGAAATTTACCTTGTGCTGCC 584
Db      421  GCCCATGGCCATGATTGAGAAATTTACCTTGTGCTGCC 458
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RESULT 9
N49208
LOCUS   N49208 452 bp mRNA linear EST 14-FEB-1996
DEFINITION yy84e08.s1 Soares multiple sclerosis 2NDHSP Homo sapiens cDNA
clone IMAGE:280262 3', mRNA sequence.
ACCESSION N49208
VERSION   N49208.1 GI:1190374
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
          1 (bases 1 to 452)
          Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
          Holman,M., Hultman,M., Kucaba,T., Le.M., Lennon,G., Marra,M.,
          Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
          Trevisan,E., Waterston,R., Williamson,A., Wohldmann,P. and
          Wilson,R.
          The WashU-Merck EST Project
          Unpublished (1995)
          Contact: Wilson RK
          Washington University School of Medicine
          4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
          Tel: 314 286 1800
          Fax: 314 286 1810
          Email: est@watson.wustl.edu
          This clone is available royalty-free through LLNL; contact the
          IMAGE Consortium (info@image.llnl.gov) for further information.
          Possible reversed clone: polyT not found
          Seq primer: m13 -40 forward
          High quality sequence stop: 390.
FEATURES
source    Location/Qualifiers
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            /mol_type="mRNA"
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/db_xref="GDB:3898638" /db_xref="taxon:9606" /clone="IMAGE:280262" /sex="male" /tissue_type="multiple sclerosis lesions" /dev_stage="Age 46" /lab_host="DH10B (ampicillin resistant)" /clone_lib="Soares multiple sclerosis 2NDHMSp" /note="Vector: p7T3D (Pharmacia) with a modified polylinker V TYPE: phagemid; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5], TGTTACCAATCTGAAGTCGGAGCGCGCATTTTTTTTTTTTTTTT 3', double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified p7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M. Fatima Bonaldo. RNA from 4 multiple sclerosis lesions from one patient was kindly provided by Dr. Kevin G. Becker (NINDS/NIH). "		ORIGIN		Query Match 70.8%; Score 413.6; DB 7; Length 452; Best Local Similarity 98.5%; Pred. No. 7.1e-91; Matches 445; Conservative 0; Mismatches 4; Indels 3; Gaps 2;	
QY	1	GGGNCGGCGNNGNGCAAGGTGCTGAGCGCCCTCCTAGNGCCTCCCTTTCGCGCCTCCCTCC 60			
DB	1	GGGNCGGCGNNGNGCAAGGTGCTGAGCGCCCTCCTAGNGCCTCCCTTTCGCGCCTCCCTCC 60			
QY	61	TCTGCCCGCCGTAGCAGTGACATGCGGTGTGGAGGTAGATGGCTTCCCGCGCGGAG 120			
DB	61	TCTGCCCGCCGTAGCAGTGACATGCGGTGTGGAGGTAGATGGCTTCCCGCGCGGAG 120			
QY	121	GGCGGGTGGATCGCGCGCTGGGAGAGCAGCGCCGATTCAGCTGCCCGCGCGCC 180			
DB	121	GGCGGGTGGATCGCGCGCTGGGAGAGCAGCGCCGATTCAGCTGCCCGCGCGCC 180			
QY	181	CGGCGACCTTGGAGTCCCGGTTCAGCGCATGGGGACCTCTCCAGCAGCAGCAGCGCC 240			
DB	181	CGGCGACCTTGGAGTCCCGGTTCAGCGCATGGGGACCTCTCCAGCAGCAGCAGCGCC 240			
QY	241	TGCGCTCTCGAGCGCATCGCCCGCGAGCCACAGCAGATGATCGCGGGTCCCTTC 300			
DB	241	TGCGCTCTCGAGCGCATCGCCCGCGAGCCACAGCAGATGATCGCGGGTCCCTTC 300			
QY	301	TCTGCTTGGATTCCTTAGCACCACACAGCTCAGCAGAAACAGAGCGCTCGAATCTCA 360			
DB	301	TCTGCTTGGATTCCTTAGCACCACACAGCTCAGCAGAAACAGAGCGCTCGAATCTCA 360			
QY	361	TT-GGCACATACCGCATGTTGACCGTSCCACCAGCGAGTGCTAACT--GTGACAAGT 417			
DB	361	TTGGGCACATACCGCATGTTGACCGTSCCACCAGCGAGTGCTAACTTTGTGACAAGT 420			
QY	418	GTCCAGCAGGAACCTATGCTCTGAGCATTTGT 449			
DB	421	GTCCAGCAGGAACCTATGCTCTGAGCATTTGT 452			
RESULT 10 BE049432 LOCUS		503 bp mRNA linear EST 08-JUN-2000 xw86d09.x1 NCI CGAP Pani Homo sapiens cDNA clone IMAGE:2834897 3', similar to TR_075509 075509 TNFR-RELATED DEATH RECEPTOR-6. ; contains PTR5.t2 PTR5 PTR5 repetitive element ;, mRNA sequence.			
ACCESSION VERSION KEYWORDS SOURCE ORGANISM		BE049432.1 GI:8366487 Homo sapiens (human)			

Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Soabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

Direct Submission

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: <http://genome.gsc.riken.jp/>, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL: <http://genome.gsc.riken.jp/>

URL: <http://fantom.gsc.riken.jp/>

FEATURES
source

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/organism="Mus musculus"
/locus_tag="Mm004418220.1"
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/strain="C57BL/6J"
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445. .2412
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mutative"

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TENDVRKCCARTGSDVSPSSVMKCAHTDCLQNLEVVKPGTKETDNGCMRLFTF
STNPSSGTYTFSPHEMHESHDPSTYEPQGMNSTDNSTSVARTKVPSGIEBGTVP
DNTSSGKEGTNRNLPNPOVTHQAAPHRIHLKLLPSMWEATGKXSATIAKPAKGA
HPRNAUKHFDINHLHPWMI VLFLLVLIVTCSIRKSSRTIKCPQDPSPASIVKGA
GLKSLTPQNRKXKI YNRNGHGDILUKAAVQSGOWKDIYOPLCNARSREVAAFSN
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3608..3613
3628
/notes="putative"

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	Query Match	65.9%	Score 385;	DB 3;	Length 3628;
	Best Local Similarity	82.0%;	Pred. No. 9.9e-84;		
	Matches 493;	Conservative 0;	Mismatches 91;	Indels 17;	Gaps 4;
QY	1	GCNC CGCNGNNGNC AAGGTGCTGAGCGCCCT-AGNGCCTCCCTTGCGCCTCCCTC	59		
Db	219	GCGCCACGCGCCCTGGCGAGGTGCTGAGCGCTTTCGGAGCCTCCCTGCTGCTCCCTC	278		
QY	60	CTC-----TGCCCGCCGTAGCAGTGACACATGGGGTGTGGAGGTAGATGGGCT-C	110		
Db	279	TTCCGCGCTGGGTGCTGCTGCTGAGTGACATGGGCTGCTGGAGGTAGTGGGCTCAC	338		
QY	111	CGSCCGGAGCGCGCGGTGGATCGGCCCTGGGCAGAGCAGCGCCGATTCACAGCTGCC	170		
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/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Pr50"
/notes="Organ: prostate; Vector: PCMV-SPORT6.1; Site 1:
NotI; Site 2: EcoRV; Cloned unidirectionally, primer:
Oligo dt. Pool of 3 primary libraries: NCI_CGAP_Pr39
(dorsolateral prostate from 11 wk male, 3 days
post-castration, average insert size 2.7 kb),
NCI_CGAP_Pr29 (dorsolateral prostate from 11 wk male, 5
days post-castration, average insert size 2.2 kb) and
NCI_CGAP_Pr42 (dorsolateral prostate from 11 wk male, 7
days post-castration, average insert size 2.2 kb).
Constructed by Life Technologies/Invitrogen. Note: this is
a NCI CGAP library."

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ORIGIN

Query Match	65.9%	Score 384.6	DB 6	Length 645
Best Local Similarity	82.0%	Pred. No. 9.8e-84		
Matches 493	Conservative 0	Mismatches 90	Indels 18	Gaps 4
QY	1	GCNCGCGNNGNGCAAGGTGCTGAGCCG--CCTAGNGCCTCCCTTCGCGGCTCCCT	58	
Db	45	GCGCCAGCGCCCTGGGACAGTGTCTGAGCGCTTCTCCGAGCTCCCTGCTGCTCCCT	104	
QY	59	CCTCTGCCCGGCC-----GTAGCAGTGCAATGSGGTGTTGGAGGTAGATGGGCTC-	109	
Db	105	CTTCGCGCTAGCGCCTTGCTGTCTGCTAGTGCAATGGGCTCTGGAGGTAGATGGGCTCA	164	
QY	110	CCGGCCGGGAGGGGGGTGGATGCGCGCTGTGGCGAGAAGCAGCGCGCGATTCACAGTCG	169	
Db	165	CCGCGCGTAGGGCGGGTGTGATCGGCGCTGGGCGAANAACAGCCACCGATTCCAGCTGC	224	
QY	170	CCGCGG-----CGCCCCGGGCACCTTTCGAGTCTCCCGTTTCAGCCATGGGACCTCTC	222	
Db	225	CGTGGGGCCGAGCGCCCGGAGCGCGCTGCGAGCCCGGCTCAGCCATGGGACCTCCG	284	
QY	223	CGAGCAGCAGCAGCGCCCTCGCTCTCTGACGCCGATCGCCCGGAGCCACAGCCACGA	282	
Db	285	CAAGCAGCATCACCGCCCTCGCTCTTTCAGCGCGCATCGCCGGCAAAGTTGGAGCCACGA	344	
QY	283	TGATCGGGGCTCCCTTCTCTGCTTGGATTCTTAGCACACACACAGCTCAGCAGAAC	342	
Db	345	TGCTCGCGGCTCCCTTCTCTGCTTGGTTCTCAGCACATCAGCCCAACAGAAC	404	
QY	343	AGAAGGCTCGAATCTCATTTGGCACATACCGCCCATGTTGACCGTGCCACCGGCCAGGTGC	402	
Db	405	AAAAGACTCTGAGTCTCACGGGCAGGTACCGCACGTTGACCGTACCCTGGCCAGGTGC	464	
QY	403	TAACTGTGACAGTGTCCAGCAGGAACCTATGTCTCTGAGCATTTGACCAACACAGCC	462	
Db	465	TAACTTCGCAACAAGTGTCCGGCAGGAACGTATGTCTCCGAGCATGTGACCAACACAGCC	524	
QY	463	TGCGGTCTCCAGCATGTCCCTGTGGGACCTTTACAGGCATGAGAAATGGCATAGAGA	522	
Db	525	TGGAGTCTCCAGCAGCTGCCCTCGGGGACCTTTACAGGCATGAGAACGGCATAGAGA	584	
QY	523	AATGCCATGACTGTAGTCAGCCATGCCCATGGCCAAATGATTGAGAAATTAACCTTGTGCTG	582	
Db	585	GATGCCATGACTGTAGTCAGCCATGCCCAACGGCCGATGATTGAGAGATTACCTTGTGCTG	644	
QY	583	C	583	
Db	645	C	645	

RESULT 14	AA918818	420 bp	linear	EST 10-JUN-1998
LOCUS	AA918818			
DEFINITION	c169609.s1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:153488 3', mRNA			
ACCESSION	AA918818			
VERSION	AA918818.1			
KEYWORDS	GI:3058708			
SOURCE	EST.			
	Homo sapiens (human)			

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 420)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/abbrp/image.html
Insert Length: 3337 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence spot: 401.

FEATURES

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/clone="IMAGE:153488"
/lab_host="DH10B"
/clone_lib="NCI CGAP Kid3"
/note="organ: kidney; Vector: p7T3D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer,
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified p7T3 vector. mRNA
source: 2 pooled kidneys. Library went through one round
of normalization. Library constructed by Bento Soares and
M. Fatima Bonaldo."

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ORIGIN

Query Match	65.5%	Score	382.6	DB 1	Length	420			
Best Local Similarity	97.2%	Pred. No.	2.9e-83						
Matches	410	Conservative	0	Mismatches	10	Indels	2	Gaps	2
QY	30	GC	CCCTAGAGCCTCCCTTGC	CGCCTCCCTCTCTG	CCCGCGCGGTAG	CAGTGCACATGGGG	89		
DB	1	GC	CCCTAGAGCCTCCCTTGC	CGCCTCCCTCTCTG	CCCGCGCGGTAG	CAGTGCACATGGGG	60		
QY	90	TG	TGTGAGGTAGATGGCTCC	CGGCGCGGAGCGG	CGGTGGATG	CGCGCTGGGCGAGAAG	149		
DB	61	TG	TGTGAGGTAGATGGCTCC	CGGCGCGGAGCGG	CGGTGGATG	CGCGCTGGGCGAGAAG	120		
QY	150	CAG	CGCCGATTCACAGTGC	CGCGCGCGCCCGGCC	CACCTTGC	GAGTCCCGGTTTCAGCC	209		
DB	121	CAG	CGC-CGATTCACAGTGC	CGCGCGCGCCCGGCC	CCCTTG	CGAGTCCCGGTTTCAGCC	179		
QY	210	AT	GGGACCTCTCCGAGCAG	CAGCACCGCCTCG	CTCTG	CAGCGCATCGCCCGCCGGA	269		
DB	180	AT	GGGACCTCTCCGAGCAG	CAGCACCTCC	CTCG	CAGCAGCATCGCCCGCCGGA	239		
QY	270	GC	CACAGCCAGATGATCG	GGGCTCGCTTCTCTG	GATTCCTT	GAGTCCCTAGCACCCACA	329		
DB	240	GC	CACAGCCATGATGATCG	GGGCTCCCATCTCT	CTG	ATTCCTTAGCACCCACA	289		
QY	330	GCT	CAGCCAGAACAGAA	GGCCTCGAATCTCAT	TGGCACATAC	CGCCATGTGTGACCGTGC	389		
DB	300	GCT	CAGCCAGAACAGAA	GGCCTCGAATCTCAT	TGGCACATAC	CGCCATGTGTGACCGTGC	359		
QY	390	AC	CGGCGAGGTGTACCT	TGTGACAGTGTCC	AGCAGGACCTAT	CTCTGTGACCATGT	449		
DB	360	AC	CGG-CAGGTGCTCAACT	TGTGACAGTGTCC	AGCAGGACCTAT	GTCTCTGACCATGT	418		
QY	450	AC	451						

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Db      419 AC 420
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RESULT 15
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LOCUS      497 bp      mRNA      linear      EST 04-SBP-2003
DEFINITION DKFZp761B2115 x1 761 (synonym: hamy2) Homo sapiens cDNA clone
KEYWORDS   DKFZp761B2115-5', mRNA sequence.
ACCESSION  AL138519
VERSION    AL138519
SOURCE     AL138519.1 GI:6862557
ORGANISM   Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 497)
AUTHORS   Ansorge,W., Wirkner,U., Mewes,H.W., Weil,B. and Wiemann,S.
TITLE     EST (Ansorge,W., Wirkner,U., Mewes,H.W., Weil,B. and Wiemann,S.)
JOURNAL   Unpublished (1999)
COMMENT   Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by EMBL (European Molecular Biology Laboratories,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No sl sequence available.
This clone (DKFZp761B2115) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES             Location/Qualifiers
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ORIGIN

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Query Match      63.7%; Score 372; DB 1; Length 497;
Best Local Similarity 93.9%; Pred. No. 1.2e-80;
Matches 443; Conservative 0; Mismatches 20; Indels 9; Gaps 5;

QY      74  AGCAGTGCACATGGGGTGTGGAGGTAGATGGGCTCCCGG-CCGGGAGGCGCGGTGGAT 132
Db      1  AGCAGTGCACATGGGGTGTGGAGGTAGATGGGCTCCCGGCGCGGAGGCGCGGTGGAT 60
QY      133 CGGCGCTGGGCGAGACAGCGCGGATTCAGCTGCCCGCGCGCCCG-GGCCACCTTG 191
Db      61  CGGCGCTGGGCGAGACAGCGCGGATTCAGCTGCCCGCGCGCCCGCGCGCGCTG 120
QY      192 CGAGTCCC CGGTTTCAGCATGGGACCTCTCCGAGCAGCAGCAGCGCCCTCGCCTCTCTGC 251
Db      121 CAATTCCCGGTTTCAGCCATGGGACCTCTCCGAGCAGCAGCAGCGGCGCTGCTCTCTGC 180
QY      252 AGCGGCATCGCGCGCGAGCAGCAGCAGCATGATCGCGGCTCCCTTCTCTGCTTGA 311
Db      181 AGCGGCATCGCGCGCGAGCAGCAGCAGCATGATCGCGGCTCCCTTCTCTGCTTGA 240
QY      312 TTCTTTAGCACCAACACAGCTCAGCCAGAACAGAGGCGCTCGAATCTCATTGGCACAATAC 371
Db      241 TTCTTTAGCACCAACACAGCTCAGCCAGAACAGAGGCGCTCGAATCTCATTGGCACAATAC 300
QY      372 CGCCATGTTGACCGTGCACCGGCGAGGTGCTAACCTGTGACAGTGTCCAGCAGGAACC 431
Db      301 CGCCATGTTGACCGTGCACCGGCGAGGTGCTAACCTGTGACAGTGTCCAGCAGGAACC 360
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QY      432 TATGTCCTGAGCATTGTACCAACACAGCCTGCGGCTCTGCAGCAGTTGCCCTGTGGGG 491
Db      361 TATGTCCTGAGCATTGTAC--AACACAGCCTGCGGCTCTGCAGCAGTTGCC--TGTGG 415
QY      492 ACCTTTACCAGGCATGAGAAATGGCATAGAGAAATGCCATGACTGTGTAGTCAGC 543
Db      416 GACCTTACCAGGCATGATGGCATAGAGAA--TGCATGACTGTGTAGTCAGC 465

Search completed: January 8, 2005, 03:53:42
Job time : 3440 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 7, 2005, 23:48:58 ; Search time 3738 Seconds
(without alignments)
7388.225 Million cell updates/sec

Title: US-10-663-157-3

Perfect score: 584

Sequence: 1 ggcncgcgngngngcaag.....agaaataacctgtgtgtgcc 584

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb.ba.*

2: gb.htg.*

3: gb.in.*

4: gb.om.*

5: gb.ov.*

6: gb.pat.*

7: gb.ph.*

8: gb.pl.*

9: gb.pr.*

10: gb.ro.*

11: gb.sts.*

12: gb.sy.*

13: gb.un.*

14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	578	99.0	584	E29453	Tumor necro
2	578	99.0	584	AR437901	Sequence
3	576.4	98.7	2271	BD263012	Nucleic a
4	571.6	97.9	1686	BD263011	Nucleic a
5	570	97.6	1686	BD263014	Nucleic a
6	550.2	94.2	588	AR437902	Sequence
7	544.8	93.3	2636	AX876881	Sequence
8	544.8	93.3	2636	BD156366	Primer fo
9	544.8	93.3	2636	AK001504	Homo sapi
10	544.8	93.3	2638	AR134339	Sequence
11	544.8	93.3	2638	BD076495	Novel mol
12	544.8	93.3	2877	BD235207	Mammalian
13	544.8	93.3	3474	BD271797	Human tum
14	544.8	93.3	3474	AR200579	Sequence
15	544.8	93.3	3474	AR441939	Sequence
16	544.8	93.3	3474	BD124556	Human tum
17	543.2	93.0	3534	CQ767596	Sequence
18	543.2	93.0	3534	AX376350	Sequence
19	543.2	93.0	3534	AY358304	Homo sapi

20	529.4	90.7	2612	6	AR134328	Sequence
21	529.4	90.7	2612	6	BD076484	Novel mol
22	528.8	90.5	1031	6	BD235206	Mammalian
23	405	69.3	3277	6	BD261788	Tumor nec
24	386.6	66.2	2748	10	BC016420	Mus muscu
25	386	66.1	773	6	BD263013	Nucleic a
26	386	66.1	3238	9	BC017730	Homo sapi
27	381	65.2	2186	6	E29452	Tumor necro
28	381	65.2	2186	6	AR437900	Sequence
29	380	65.1	3236	6	BD261794	Tumor nec
30	375	64.2	759	6	AR134330	Sequence
31	375	64.2	759	6	BD076486	Novel mol
32	375	64.2	1474	6	BD235208	Mammalian
33	375	64.2	1815	6	AR134340	Sequence
34	375	64.2	1815	6	BD076496	Novel mol
35	375	64.2	1965	6	BD261789	Tumor nec
36	375	64.2	1968	6	AX327471	Sequence
37	375	64.2	1968	6	AX582233	Sequence
38	375	64.2	1968	6	AX706993	Sequence
39	375	64.2	1968	9	AF068868	Homo sapi
40	375	64.2	1968	9	BT007420	Homo sapi
41	375	64.2	1968	12	BT009883	Synthetic
42	303	51.9	1893	6	BD261790	Tumor nec
43	302.8	51.8	2393	6	BD263015	Nucleic a
44	299.8	51.3	1968	10	AY043489	Mus muscu
45	298.2	51.1	1968	10	AF322069	Mus muscu

ALIGNMENTS

RESULT 1	E29453	584 bp	DNA	linear	PAT 18-JUN-2001
LOCUS	E29453				
DEFINITION	Tumor necrosis-associated receptor TR7.				
ACCESSION	E29453				
VERSION	E29453.1	GI:13025565			
KEYWORDS	JP 1999018786-A/2.				
SOURCE	unidentified				
ORGANISM	unclassified.				
REFERENCE	1 (bases 1 to 584)				
AUTHORS	Keith, C.D., Mark, R.H., Peter, Y. and K.B.T.				
TITLE	Tumor necrosis-associated receptor TR7				
JOURNAL	Patent: JP 1999018786-A 2 26-JAN-1999;				
COMMENT	SMITHKLINE BEECHAM CORP				
	OS Unidentified				
	PN JP 1999018786-A/2				
	PD 26-JAN-1999				
	PF 02-APR-1998 JP 1998126559				
	PR 02-APR-1997 US 60/041796-28-OCT-1997 US 08/959382 PI				
	KEITH C DEAN, MARK R HURLE, PETER YOUNG, K B TAN PC				
	C12N15/09, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K45/00, PC				
	A61K48/00,				
	PC C07K14/705, C07K16/30, C12N1/15, C12N1/19, C12N1/21, C12N5/10, PC				
	C12N5/10,				
	PC				
	C12P21/02, G01N33/53, G01N33/531, G01N33/566, G01N33/577, C12N15/00, PC				
	A61K37/02,				
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Best Local Similarity 100.0%; Pred. No. 2.1e-108;
Matches 584; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 181 CGGCGACCTTGCAGTCCCGGTTTCAGCCATGCGGACCTCTCCGAGCAGCAGCGGCC 240
Db 181 CGGCGACCTTGCAGTCCCGGTTTCAGCCATGCGGACCTCTCCGAGCAGCAGCGGCC 240

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Db 241 TGCGCTTCCTGACCGCGATCGCGCCCGCGGATTCAGCTGCGCGCGGCCCTCCCTTC 300

QY 301 TCCTGCTTGGATTCTTAGCACCACTAGCGGAGAGAGAGGCTCGAATCTCA 360
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QY 541 AGCCATGCCATGGCAATGATTGAGAAATACCTTGTGCTGCC 584
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RESULT 2
LOCUS AR437901 AR437901 584 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 3 from patent US 6660839.
ACCESSION AR437901
VERSION AR437901.1 GI:40203125
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 584)
AUTHORS Deen,K.C., Hurlle,M.R., Young,P. and Tan,K.B.
TITLE Tumor necrosis related receptor, FR7
JOURNAL Patent: US 6660839-A 3 09-DEC-2003;
FEATURES
source Location/Qualifiers
1..584 /organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 99.0%; Score 578; DB 6; Length 584;
Best Local Similarity 100.0%; Pred. No. 2.1e-108;
Matches 584; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGNCCGCGNGNGNGCAAGTCTGTAGCGCCCTTAGNGCTCCCTTGGCGCTCCCTCC 60
Db 1 GCGNCCGCGNGNGNGCAAGTCTGTAGCGCCCTTAGNGCTCCCTTGGCGCTCCCTCC 60

QY 61 TCTGCCCGCGGTAGCAGTGCACATGGGGTGTGGAGGTAGATGGGCTCCCGCGCGGAG 120
Db 61 TCTGCCCGCGGTAGCAGTGCACATGGGGTGTGGAGGTAGATGGGCTCCCGCGCGGAG 120

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Db 121 GCGGCGGTGAGATCGGCGCTGGGAGAGCAGCGCGGATTCAGCTGCGCGCGGCC 180

QY 181 CGGCGACCTTGCAGTCCCGGTTTCAGCCATGCGGACCTCTCCGAGCAGCAGCGGCC 240
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QY 301 TCCTGCTTGGATTCTTAGCACCACTAGCGGAGAGAGAGGCTCGAATCTCA 360
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QY 541 AGCCATGCCATGGCAATGATTGAGAAATACCTTGTGCTGCC 584
Db 541 AGCCATGCCATGGCAATGATTGAGAAATACCTTGTGCTGCC 584

RESULT 3
LOCUS BD263012 BD263012 2271 bp DNA linear PAT 17-JUL-2003
DEFINITION Nucleic acids encoding osteoprotegerin-like proteins and methods of using same.
ACCESSION BD263012
VERSION BD263012.1 GI:33072780
KEYWORDS JP 2002528067-A/2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 2271)
AUTHORS Shimkets,R.A., Yang,M., Lichenstein,H. and McDonald,W.F.
TITLE Nucleic acids encoding osteoprotegerin-like proteins and methods of using same
JOURNAL Patent: JP 2002528067-A 2 03-SEP-2002;
COMMENT CURAGEN CORP
OS Homo sapiens (human)
PN JP 2002528067-A/2
PD 03-SEP-2002
PF 22-OCT-1999 JP 2000578341
PR 23-OCT-1998 US 60/105481.01-OCT-1999 US 60/156993 PR
21-OCT-1999 US 09/422680
PI RICHARD A SHIMKETS,MEIJIA YANG,HENRI LICHENSTEIN,WILLIAM F PI
MCDONALD
PC C12N15/09,A61K31/711,A61K38/00,A61K38/22,A61K39/395,A61K45/00,
PC A61P19/00,
PC A61P19/08,A61P19/10,A61P43/00,C07K14/51,C07K16/22,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,C12P12/08,C12N15/00,C12N5/00,A61K37/02, PC
A61K37/24
CC wherein any n is an a, t, c or g
FH Key Location/Qualifiers
FT CDS (102)..(2174)
FT misc feature (3)..(37).
FT Location/Qualifiers

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ORIGIN
Query Match 98.7%; Score 576.4; DB 6; Length 2271;
Best Local Similarity 99.8%; Pred. No. 4e-108;
Matches 583; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 61 TCTGCCCGCGGTAGCAGTGCACATGGGGTGTGGAGGTAGATGGGCTCCCGCGGGAG 120
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QY 121 GCGGCGGTGATCGGCGCTGGGAGAGAGCGCGGCGGATTCAGCTGCCCGCGGGCCC 180
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DB 241 TCGCCTCTCGAGCGCATCGCCGCGGAGCCACAGCAGATGATCGGGGCTCCCTTC 300
QY 301 TCTGCTTGATTCCTTAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGTCA 360
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QY 361 TTGSCACATACCGCATGTTGACCTGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGT 420
DB 361 TTGSCACATACCGCATGTTGACCTGCGCAGCAGCAGCAGCAGCAGCAGCAGT 420
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QY 541 AGCCATGCCCATGGCCAAATGATTGAGAAATACCTTGTGTGCTGCC 584
DB 541 AGCCATGCCCATGGCCAAATGATTGAGAAATACCTTGTGTGCTGCC 584

RESULT 4
BD263011 1686 bp DNA linear PAT 17-JUL-2003
LOCUS Nucleic acids encoding osteoprotegerin-like proteins and methods of
DEFINITION using same.
ACCESSION BD263011.1 GI:33072779
KEYWORDS JP 2002528067-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Shimkets,R.A., Yang,M., Lichenstein,H. and Mcdonald,W.F.
JOURNAL Nucleic acids encoding osteoprotegerin-like proteins and methods of
Patent: JP 2002528067-A 1 03-SEP-2002;
CURAGEN CORP
COMMENT OS Homo sapiens (human)
PN JP 2002528067-A/1
PD 03-SEP-2002
PF 22-OCT-1999 JP 2000578341

PR 23-OCT-1998 US 60/105481,01-OCT-1999 US 60/156993 PR
21-OCT-1999 US 09/422680
PI RICHARD A SHIMKETS,MEIJIA YANG,HENRI LICHENSTEIN,WILLIAM F PI
MCDONALD
PC C12N15/09,A61K31/711,A61K38/00,A61K38/22,A61K39/395,A61K45/00,
PC A61P19/00,
PC A61P19/08,A61P19/10,A61P43/00,C07K14/51,C07K16/22,C12N1/15, PC
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A61K37/24
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FH Key Location/Qualifiers
FT CDS (102)..(971)
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Matches 579; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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LOCUS Nucleic acids encoding osteoprotegerin-like proteins and methods of
DEFINITION using same.
ACCESSION BD263014
KEYWORDS JP 2002528067-A/1
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Shimkets,R.A., Yang,M., Lichenstein,H. and Mcdonald,W.F.
JOURNAL Nucleic acids encoding osteoprotegerin-like proteins and methods of
Patent: JP 2002528067-A 1 03-SEP-2002;
CURAGEN CORP
COMMENT OS Homo sapiens (human)
PN JP 2002528067-A/1
PD 03-SEP-2002
PF 22-OCT-1999 JP 2000578341
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KEYWORDS JP 2002528067-A/4.
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1686)
 AUTHORS Shimkets, R.A., Yang, M., Lichenstein, H. and McDonald, W.F.
 TITLE Nucleic acids encoding osteoprotegerin-like proteins and methods of
 using same
 JOURNAL Patent: JP 2002528067-A 4 03-SEP-2002;
 CURAGEN CORP
 COMMENT OS Homo sapiens (human)
 PN JP 2002528067-A/4
 PD 03-SEP-2002
 PP 22-OCT-1999 JP 2000578341
 PR 23-OCT-1998 US 60/105481, 01-OCT-1999 US 60/156993 PR
 21-OCT-1999 US 09/422680
 PI RICHARD A SHIMKETS, MEIJIA YANG, HENRI LICHENSTEIN, WILLIAM F PI
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 PC C12N15/09, A61K31/711, A61K38/00, A61K38/22, A61K39/395, A61K45/00,
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 PC A61P19/08, A61P19/10, A61P43/00, C07K14/51, C07K16/22, C12N1/15, PC
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 A61K37/24
 CC Nucleic acids encoding osteoprotegerin-like proteins and CC
 methods of using
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FEATURES

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ORIGIN

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 QY 1 GCGNCCGCGNNGNGCAAGGTGCTGAGCGCCCTAGNGCCTCCCTTGGCGCTCCCTCC 60
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 DEFINITION Sequence 5 from patent US 6660839.
 ACCESSION AR437902
 VERSION AR437902.1 GI:40203126
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 588)
 AUTHORS Deen, K.C., Hurler, M.R., Young, P., and Tan, K.B.
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 JOURNAL Patent: US 6660839-A 5 09-DEC-2003;
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DEFINITION Sequence 11786 from Patent EP1074617.
ACCESSION AX876881
VERSION   AX876881.1  GI:40031617
KEYWORDS  Homo sapiens (human)
SOURCE    Homo sapiens
ORGANISM  Homo sapiens
REFERENCE
AUTHORS   Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
          Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
TITLE     Primers for synthesizing full-length cDNA and their use
JOURNAL   Patent: EP 1074617-A 11786 07-FEB-2001;
          Research Association for Biotechnology (JP)
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          Query Match      93.3%; Score 544.8; DB 6; Length 2636;
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          DEFINITION Primer for synthesizing full-length cDNA and use thereof.
          ACCESSION BD156366
          VERSION   BD156366.1  GI:27862124
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          ORGANISM  Homo sapiens
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          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
          REFERENCE 1 (bases 1 to 2636)
          AUTHORS   Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
          Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
          TITLE     Primer for synthesizing full-length cDNA and use thereof
          JOURNAL   Patent: JP 2002191363-A 11209 09-JUL-2002;
          HELIX RESEARCH INSTITUTE
          COMMENT    OS Homo sapiens (human)
          PN JP 2002191363-A/11209
          PD 09-JUL-2002
          PF 28-JUL-2000 JP 2002280990
          PI TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,KOJI HAYASHI,KAORU
          PI JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU,
          PI KEIICHI NAGAI,TETSUJI OTSUKI
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          Query Match      93.3%; Score 544.8; DB 6; Length 2636;
          Best Local Similarity 97.4%; Pred. No. 1.2e-101;
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          QY 1 GCGNCCCGGNGNGCAAGGTGCTGAGCGCCCTAGNGCCTCCCTTGGCGCTCCCTCC 60
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RESULT 9

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 LOCUS Homo sapiens cDNA FLJ10642 fis, clone NT2RP2005752, highly similar
 DEFINITION to Homo sapiens TNFR-related death receptor-6 mRNA.

ACCESSION

AK001504.1 GI:7022799

VERSION

oligo capping; fis (full insert sequence).

KEYWORDS

Homo sapiens (human)

SOURCE

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R., Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H., Sekine, M., Yamamoto, M., Nishi, T., Shibahara, T., Tanaka, T., Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y., Nagahara, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuma, M., Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T., Kikkawa, E., Omura, Y., Abe, K., Kamihara, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M., Ninomiya, K., Ishibashi, T., Yamashita, H., Murakawa, K., Fujimori, K., Tanai, H., Kimata, M., Watanabe, M., Hiraoka, S., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, S., Yosida, M., Hotuta, T., Kusano, J., Kanehori, K., Takahashi-Fujii, A., Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R., Takeuchi, K., Arita, M., Imose, N., Musashino, K., Yuuki, H., Oshima, A., Sasaki, N., Aotsuka, S., Yoshihara, Y., Matsunawa, H., Ichihara, T., Shiohata, N., Sano, S., Moriya, S., Momiyama, H., Satoh, N., Takami, S., Terashima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H., Terahashi, Y., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, T., Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukutami, Y., Fujimori, Y., Komiyama, M., Tashiro, H., Tanigami, A., Fujiiwara, T., Ono, T., Yamada, K., Fujii, Y., Ozaki, K., Hirao, M., Ohmori, Y., Kawabata, A., Hikiji, T., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Kawakami, T., Noguchi, S., Itoh, T., Shigetani, K., Senba, T., Matsumura, K., Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togashi, T., Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J., Satoh, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K., Nagase, T., Nomura, N., Kikuchi, H., Masuho, Y., Yamashita, R., Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T. and Sugano, S. Complete sequencing and characterization of 21,243 full-length human cDNAs

Nat. Genet. 36 (1), 40-45 (2004)

JOURNAL

PUBLISHED 14702039

REFERENCE

2 Isogai, T., Ota, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y.,

Nishikawa, T., Nagai, K., Sugano, S., Iehibashi, T., Fujimori, K., Tanai, H., Kimata, M., Watanabe, M., Hiraoka, S., Ishii, S., Kawai, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagahara, K., Masuho, Y. and Kanehori, K.
 NEDO human cDNA sequencing project
 Unpublished
 3 (bases 1 to 2636)
 Isogai, T. and Otsuki, T.
 Direct Submission
 Submitted (16-FEB-2000) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
 NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing; Research Association for Biotechnology; cDNA library construction; 5'- & 3'-end one pass sequencing and clone selection; Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.

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 Best Local Similarity 97.4%; Pred. No. 1.2e-101;
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 QY 61 TCTGCGCGCGCGCTAGCAGTGCATCGGGGTGTGTGAGGTAGATGGCTCCCGG-CGCGGA 119
 Db 244 TCTGCGCGCGCGCAGCAGTGCATCGGGGTGTGTGAGGTAGATGGCTCCCGGCGCGGA 303
 QY 120 GCGGCGGTGTGATGCGGCGCTGGGCGAAGAGCGCGCGATTCAGCTGCCCGCGCGCC 179
 Db 304 GCGGCGGTGTGATGCGGCGCTGGGCGAAGAGCGCGCGATTCAGCTGCCCGCGCGCC 363
 QY 180 CC-GGCCACCTTTCGAGTCCCGGTTTCAGCATGGGACCTCTCCGAGCAGCAGCAGCCG 238
 Db 364 CCGGGCGCGCCCTTCGAGTCCCGGTTTCAGCATGGGACCTCTCCGAGCAGCAGCAGCCG 423
 QY 239 CTTGCGCTCTCTGAGCGCGATCGCCCGCGAGCCACAGCAGATGATCGCGGGTCCCT 298
 Db 424 CTTGCGCTCTCTGAGCGCGATCGCCCGCGAGCCACAGCAGATGATCGCGGGTCCCT 483
 QY 299 TCTCTGTCTTGGATCTTTAGCACCACCAAGCTCAGCCAGAACAGAGGCTTCGAATCT 358
 Db 484 TCTCTGTCTTGGATCTTTAGCACCACCAAGCTCAGCCAGAACAGAGGCTTCGAATCT 543
 QY 359 TTTTGGCAGATACCGCCATGTTGACCGTGCACCGCGGAGGTGCTAACTGTGACAGTG 418
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LOCUS AR134339
DEFINITION Sequence 22 from patent US 6194151.
ACCESSION AR134339
VERSION AR134339.1
KEYWORDS AR134339.1 GI:14123244
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2638)
AUTHORS Busfield,S.J.
TITLE Molecules of the TNF receptor superfamily and uses therefor
JOURNAL Patent: US 6194151-A 22 27-FEB-2001;
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    Best Local Similarity 97.4%; Pred. No. 1.2e-101;
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Db |||
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RESULT 11
LOCUS BD076495
DEFINITION Sequence 22 from patent US 6194151.
ACCESSION BD076495
VERSION BD076495.1
KEYWORDS BD076495.1 GI:22622098
SOURCE Unidentified.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2638)
AUTHORS Busfield,S.J.
TITLE Molecules of the TNF receptor superfamily and utilization thereof
JOURNAL Patent: JP 2001517443-A 13 09-OCT-2001;
COMMENT MILLENNIUM PHARMACEUTICALS INC
PN JP 2001517443-A/13
PD 09-OCT-2001
PF 25-SEP-1998 JP 2000512955
PR 26-SEP-1997 US 08/938896,17-MAR-1998 US 09/042785 PI
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PC G01N33/566,C12N15/00,C12N5/00
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CC Topology: Linear;
CC Novel molecules of TNF receptor super family and utilization thereof
FH Key Location/Qualifiers
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    Best Local Similarity 97.4%; Pred. No. 1.2e-101;
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RESULT 12	BD235207	LOCUS	DEFINITION	2877 bp	DNA	linear	PAT 17-JUL-2003
			Mammalian genes; dendritic cell prostaglandin-like transporter (DC-PGT), HPT6A, HSLJDP37R and RANKL, HCC5 chemokine, deubiquitinations 11 and 12 (DUB11, DUB12), MD-1, MD-2 and cyclin E2, and reagents and methods relating thereto.				

Query Match	Score	DB	Length
Best Local Similarity	93.3%	544.8	2877
Matches 571; Conservative	97.4%	Pred. NO. 1.2e-101	
		0; Mismatches 13;	
		Indels 2; Gaps 2;	

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Qy	180	CC-GGCCACCTTGGGAGTCCCGGTTTCAGCCATGGGGACCTCTCCGAGCAGCAGCACCGC	238
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Qy	479	TTGCCCTGTGGGACCTTTTACCAGGCATGAGAAATGGCATGAGAAATGCCATGCTGTAG	538
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LOCUS	Human tumor necrosis factor receptor TR9.				
DEFINITION	BD271797				
ACCESSION	BD271797.1	GI:33081565			
VERSION	JP 2002542771-A/1.				
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	Ni, J., Gentz, R.L., Yu, G.L. and Fan, P.				
AUTHORS	Human tumor necrosis factor receptor TR9				
TITLE	Patent: JP 2002542771-A 1 17-DEC-2002;				
JOURNAL	HUMAN GENOME SCIENCES INC				
COMMENT	OS Homo sapiens (human)				
	PN JP 2002542771-A/1				
	PD 17-DEC-2002				
	PF 16-MAR-2000 JP 20000606721				
	PR 24-MAR-1999 US 60/126019, 14-MAY-1999 US 60/134220 PI				
	JTAN NI, REINER L, GENTZ, GUO LIANG YU, PING FAN				
	PC C12N15/09, A61K38/00, A61K39/395, A61K39/395, A61K45/00, A61K48/00,				
	PC A61P1/04,				
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	PC A61P31/22,				
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	PC C12N1/15,				
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Qy	1	GGGCGCGGNGNGCAAGGTGCTGAGCGCCCTAGNGCCTCCCTTGGCGCTCCCTCC 60		
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Qy	61	TCTGCCCGCGGTAGCAGTGCACATGGGGTGTGGAGGTAGATGGGCTCCCGG-CCGGGA 119		
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Qy	419	TCAGCAGGAACCTATGTCTCTGAGCATTTGTACCAACACAGGCTCGGGTCTGCAGCAG 478		
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Db	516	TTGCCCTGTGGGACCTTTACAGGCAATGAGAAATGCGAATGCGCATGACTGTAG 575		
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VERSION	AR441939.1 GI:42669061			
KEYWORDS	Unknown.			
SOURCE	Unknown.			
ORGANISM	Unclassified.			
REFERENCE	1 (bases 1 to 3474)			
AUTHORS	Ni, J., Yu, G.-L., Fan, P. and Gentz, R.L.			
TITLE	Human tumor necrosis factor receptor TR9			
JOURNAL	Patent: US 6667390-A 1 23-DEC-2003;			
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Matches 571; Conservative 0; Mismatches 13; Indels 2; Gaps 2;				
Qy	1	GGGCGCGGNGNGCAAGGTGCTGAGCGCCCTAGNGCCTCCCTTGGCGCTCCCTCC 60		
Db	36	GGGCGCGCGCGCTGGGCAAGTGTGAGCGCCCTAGAGCCTCCCTTGGCGCTCCCTCC 95		
Qy	61	TCTGCCCGCGGTAGCAGTGCACATGGGGTGTGGAGGTAGATGGGCTCCCGG-CCGGGA 119		
Db	96	TCTGCCCGCGCGCAGCAGTGCACATGGGGTGTGGAGGTAGATGGGCTCCCGGCGGGGA 155		
Qy	120	GGCGGCGGTGATGCGGCGCTGGGCAAGACGAGCCCGCATTCACAGTGCCTCCGCGGCC 179		
Db	156	GGCGGCGGTGATGCGGCGCTGGGCAAGACGAGCCCGCATTCACAGTGCCTCCGCGGCC 215		
Qy	180	CC-GGCGACCTTCGAGTCCCGGTTACGCCATGGGGACCTCTCCGAGGAGCAGCACCGC 238		
Db	216	CCGGGCGCGCGCTGCGAGTCCCGGTTACGCCATGGGGACCTCTCCGAGGAGCAGCACCGC 275		
Qy	239	CCTCGCCTCTGCGAGCGCATCGCCGCGAGCCACAGCACGATGATCGCGGCTCCCT 298		
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Qy	299	TCTCTGCTTGGATTCTTTAGCACCAACAGCTCAGCCAGAACAGAGGCTTCGAATCT 358		
Db	336	TCTCTGCTTGGATTCTTTAGCACCAACAGCTCAGCCAGAACAGAGGCTTCGAATCT 395		
Qy	359	CATTGGCACATACCGCCATGTTGACCGTGCACCGCCAGGTGCTAACCTGTGCACAGTG 418		
Db	396	CATTGGCACATACCGCCATGTTGACCGTGCACCGCCAGGTGCTAACCTGTGCACAGTG 455		
Qy	419	TCAGCAGGAACCTATGTCTCTGAGCATTTGTACCAACACAGGCTCGGGTCTGCAGCAG 478		
Db	456	TCAGCAGGAACCTATGTCTCTGAGCATTTGTACCAACACAGGCTCGGGTCTGCAGCAG 515		
Qy	479	TTGCCCTGTGGGACCTTTACAGGCAATGAGAAATGCGAATGCGCATGACTGTAG 538		
Db	516	TTGCCCTGTGGGACCTTTACAGGCAATGAGAAATGCGAATGCGCATGACTGTAG 575		
Qy	539	TCAGCCATCCCATGCCCAATGATTGAGAAATACCTTGTGCTGCC 584		
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DEFINITION	Sequence 1 from patent US 6358508.			
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VERSION	AR200579.1 GI:20251467			
KEYWORDS	Unknown.			
SOURCE	Unknown.			
ORGANISM	Unclassified.			
REFERENCE	1 (bases 1 to 3474)			
AUTHORS	Ni, J., Yu, G.-L., Fan, P. and Gentz, R.L.			
TITLE	Antibodies to human tumor necrosis factor receptor TR9			
JOURNAL	Patent: US 6358508-A 1 19-MAR-2002;			
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Searched: 4134886 seqs, 2624710521 residues

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Maximum DB seq length: 2000000000

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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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23	543.2	93.0	3534	8 ACF20317	ACF20317 Human sec
24	543.2	93.0	3534	8 ACF19703	ACF19703 Human sec
25	543.2	93.0	3534	8 ACD21991	ACD21991 Human sec
26	543.2	93.0	3534	8 ACF13156	ACF13156 Human sec
27	543.2	93.0	3534	8 ACD25259	ACD25259 Human sec
28	543.2	93.0	3534	8 ACF00308	ACF00308 Human sec
29	543.2	93.0	3534	8 ACF72365	ACF72365 Novel hum
30	543.2	93.0	3534	8 ACD04889	ACD04889 Novel hum
31	543.2	93.0	3534	8 ACD18350	ACD18350 Human sec
32	543.2	93.0	3534	8 ACD08357	ACD08357 Human sec
33	543.2	93.0	3534	8 ACA88791	ACA88791 Novel hum
34	543.2	93.0	3534	8 ACA70233	ACA70233 Human sec
35	543.2	93.0	3534	8 ACD12455	ACD12455 Novel hum
36	543.2	93.0	3534	8 ACC74370	ACC74370 Human sec
37	543.2	93.0	3534	8 ACD15998	ACD15998 Human sec
38	543.2	93.0	3534	8 ACD25566	ACD25566 Novel hum
39	543.2	93.0	3534	8 ACD18043	ACD18043 Human sec
40	543.2	93.0	3534	8 ACC88330	ACC88330 Human sec
41	543.2	93.0	3534	8 ACD21684	ACD21684 Human sec
42	543.2	93.0	3534	8 ACD18751	ACD18751 Human sec
43	543.2	93.0	3534	8 ACA71677	ACA71677 Human sec
44	543.2	93.0	3534	8 ABX98361	ABX98361 Human CDN
45	543.2	93.0	3534	8 ACD14112	ACD14112 Human PRO

ALIGNMENTS

RESULT 1

AAV57442

ID AAV57442 standard; cDNA; 584 BP.

AC AAV57442;

XX 21-DEC-1998 (first entry)

XX Human tumour necrosis factor related receptor TR7 cDNA fragment.

XX Tumour necrosis factor related receptor; TR7; human; inflammation;

XX arthritis; septicemia; autoimmune disease; psoriasis;

XX inflammatory bowel disease; infection; graft-versus-host disease;

XX transplant rejection; stroke; acute respiratory disease syndrome;

XX ischaemia; restenosis; brain injury; AIDS; bone disease; cancer;

XX atherosclerosis; Alzheimer's disease; diagnosis; therapy; vaccine; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 210..584

XX FT /*tag= a

XX EP869179-A1.

XX 07-OCT-1998.

XX 01-APR-1998; 98EP-00302528.

XX 02-APR-1997; 97US-0041796P.

XX 28-OCT-1997; 97US-00959382.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX PI Deen KC, Hurle MR, Young P, Tan KB;

XX WPI; 1998-508493/44.

XX P-PSDB; AAW75793.

XX This cDNA clone codes for the N-terminal portion (see AAW75793) of a
CC novel member of the human tumour necrosis factor (TNF) receptor
CC superfamily, termed TR7 (see also AAW75792). TR7 polypeptides, (see
CC also AAW57441) are useful for diagnosing diseases or susceptibility to
CC diseases by identifying mutations in the TR7 gene using probes containing
CC the TR7 nucleotide sequence. TR7 polypeptides can be used to screen for
CC agonists and antagonists which bind the receptor. Gene therapy may be
CC used to effect endogenous TR7 polypeptide production. TR7 polypeptides
CC and polynucleotides can be administered directly as vaccines for
CC prevention of diseases. Diseases diagnosed, treated or prevented by the
CC above methods include: chronic and acute inflammation, arthritis,
CC septicemia, autoimmune diseases (e.g. inflammatory bowel disease,
CC psoriasis), transplant rejection, graft vs. host disease, infection,
CC stroke, ischaemia, acute respiratory disease syndrome, restenosis, brain
CC injury, AIDS, bone diseases, cancer (e.g. lymphoproliferative disorders),
CC atherosclerosis, and Alzheimer's disease. TR7 polynucleotides are also
CC useful for mapping the gene to a chromosome, allowing gene inheritance to
CC be studied through linkage analysis
XX
SQ Sequence 584 BP; 106 A; 200 C; 168 G; 104 T; 0 U; 6 Other;

Query Match 99.0%; Score 578; DB 2; Length 584;
Best Local Similarity 100.0%; Pred. No. 1.3e-125;
Matches 584; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGNCCGCGGNGNGCAAGTCTGAGCGCCCTAGNGCCTCCCTTGGCGCTCCCTCC 60
DB 1 GCGNCCGCGGNGNGCAAGTCTGAGCGCCCTAGNGCCTCCCTTGGCGCTCCCTCC 60
QY 61 TCTGCCCGCGGTAGCAGTGCACATGGGGTGTGGAGGTAGATGGGCTCCCGCGCGGAG 120
DB 61 TCTGCCCGCGGTAGCAGTGCACATGGGGTGTGGAGGTAGATGGGCTCCCGCGCGGAG 120
QY 121 GCGGCGGTGATGCGCGCTGGGCGAAGCAGCGCGCGATTCAGTGGCCCGCGCGCC 180
DB 121 GCGGCGGTGATGCGCGCTGGGCGAAGCAGCGCGCGATTCAGTGGCCCGCGCGCC 180
QY 181 CGGCCACCTTGCAGTCCCGGTTCAGCATGGGACCTCTCCGACGACGACCGCC 240
DB 181 CGGCCACCTTGCAGTCCCGGTTCAGCATGGGACCTCTCCGACGACGACCGCC 240
QY 241 TCGCCTCTCTGACGCGCATCGCCCGCGGACGACGACGATGATCGGGGCTCCCTTC 300
DB 241 TCGCCTCTCTGACGCGCATCGCCCGCGGACGACGACGATGATCGGGGCTCCCTTC 300
QY 301 TCTGCTTGGATTCCTTAGCACCACACAGCTCAGCCAGAACAGAGGCTCGAATCTCA 360
DB 301 TCTGCTTGGATTCCTTAGCACCACACAGCTCAGCCAGAACAGAGGCTCGAATCTCA 360
QY 361 TTGGCACAATACCGCATGTTGACCGTCCACCGCGGCGGATTAACCTGTGACAAGTGC 420
DB 361 TTGGCACAATACCGCATGTTGACCGTCCACCGCGGCGGATTAACCTGTGACAAGTGC 420
QY 421 CAGCAGGAACCTATGCTCTGAGCATTTGTACCAACAGCTCGCGCTCTGAGCAGATT 480
DB 421 CAGCAGGAACCTATGCTCTGAGCATTTGTACCAACAGCTCGCGCTCTGAGCAGATT 480
QY 481 GCCTGTGGGACCTTTACAGGATGAGAAATGGCATAGAGAAATGGCATGATGATC 540
DB 481 GCCTGTGGGACCTTTACAGGATGAGAAATGGCATAGAGAAATGGCATGATGATC 540
QY 541 AGCCATGCCATGCGCAATGATGAGAAATTAACCTGTGCTGCC 584
DB 541 AGCCATGCCATGCGCAATGATGAGAAATTAACCTGTGCTGCC 584

RESULT 2

AAA28728

ID AAA28728 standard; DNA; 2271 BP.

XX

AC AAA28728;

XX

DT 29-AUG-2000 (first entry)
XX Human osteoprotegerin-like 2 (OPGx2) DNA.
DE OPGx1; osteoprotegerin-like; DR6 TNF-related death receptor; agonist;
XX inhibitor; bone resorption; vascular calcification; apoptosis;
KW osteopathic; chromosome 6p11.1; D6S452; ss.
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH 102..2177
CDS /*tag= a
FT /product= "OPGx2"
FT
XX WO200024771-A2.
XX 04-MAY-2000.
XX 22-OCT-1999; 99WO-US024913.
XX 23-OCT-1998; 98US-0105481P.
PR 01-OCT-1999; 98US-0156993P.
PR 21-OCT-1999; 99US-00422680.
XX (CURA-) CURAGEN CORP.
XX Shinkets RA, Yang M, Lichenstein H, McDonald WF;
PI WPI; 2000-350692/30.
XX P-PSDB; AAY92846.
XX Nucleic acids encoding osteoprotegerin-like (OPGx) polypeptides, useful
PT for treating disorders associated with bone metabolism, such as
PT osteoporosis and osteopetrosis.
XX Claim 1; Fig 2; 81pp; English.
XX Osteoprotegerin-like polypeptides (OPGx) are expressed in bone, lymph
CC node, germinal B cells and kidney. There appear to be at least two splice
CC variants of this gene, a transmembrane form and an extracellular domain
CC form. Human OPGx1, 2 and 4 contain a 36 amino acid extension at their N-
CC terminal relative to the DR6 tumour necrosis factor (TNF)-related death
CC receptor. The OPGx gene has been mapped to chromosome 6p11.1, essentially
CC on top of D6S452. The OPGx polypeptides, agonists and antibodies are
CC useful in methods to inhibit osteoclast-mediated bone resorption or
CC vascular calcification and to modulate cell death (apoptosis). This is
CC useful for treating disorders associated with bone metabolism, such as
CC osteoporosis, osteopetrosis, or a condition characterized by loss of
CC bone, breakdown of tissue, or excessive resorption of bone tissue
XX
SQ Sequence 2271 BP; 518 A; 668 C; 611 G; 467 T; 0 U; 7 Other;

Query Match 98.7%; Score 576.4; DB 3; Length 2271;
Best Local Similarity 99.8%; Pred. No. 4e-125;
Matches 583; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCGNCCGCGGNGNGCAAGTCTGAGCGCCCTAGNGCCTCCCTTGGCGCTCCCTCC 60
DB 1 GCGNCCGCGGNGNGCAAGTCTGAGCGCCCTAGNGCCTCCCTTGGCGCTCCCTCC 60
QY 61 TCTGCCCGCGGTAGCAGTGCACATGGGGTGTGGAGGTAGATGGGCTCCCGCGCGGAG 120
DB 61 TCTGCCCGCGGTAGCAGTGCACATGGGGTGTGGAGGTAGATGGGCTCCCGCGCGGAG 120
QY 121 GCGGCGGTGATGCGCGCTGGGCGAAGCAGCGCGCGATTCAGTGGCCCGCGCGCC 180
DB 121 GCGGCGGTGATGCGCGCTGGGCGAAGCAGCGCGCGATTCAGTGGCCCGCGCGCC 180
QY 181 CGGCCACCTTGCAGTCCCGGTTCAGCATGGGACCTCTCCGACGACGACCGCC 240
DB 181 CGGCCACCTTGCAGTCCCGGTTCAGCATGGGACCTCTCCGACGACGACCGCC 240

Qy 241 TCGCTCTCTGAGCGCATCGCCGCGAGCCACAGCCACAGATGATCGCGGCTCCCTTC 300
AAA28724
Db 241 TCGCTCTCTGAGCGCATCGCCGCGAGCCACAGCCACAGATGATCGCGGCTCCCTTC 300
Qy 301 TCGCTCTCTGAGCGCATCGCCGCGAGCCACAGCCACAGATGATCGCGGCTCCCTTC 360
Db 301 TCGCTCTCTGAGCGCATCGCCGCGAGCCACAGCCACAGATGATCGCGGCTCCCTTC 360
Qy 361 TTGGCACAATACCGCATGTTGACCGTGCCACCGCCAGGCTGCTAACTGTGACAAGTGT 420
Db 361 TTGGCACAATACCGCATGTTGACCGTGCCACCGCCAGGCTGCTAACTGTGACAAGTGT 420
Qy 421 CAGCAGAACTATGCTCTGAGCATGTATACCAACAGCCGCTGCGGCTGAGCAGATT 480
Db 421 CAGCAGAACTATGCTCTGAGCATGTATACCAACAGCCGCTGCGGCTGAGCAGATT 480
Qy 481 GCCTGTGGGGACCTTTACCAAGCATGAGAAATACCTTGTGTGCC 540
Db 481 GCCTGTGGGGACCTTTACCAAGCATGAGAAATACCTTGTGTGCC 540
Qy 541 AGCCATGCCCATGCGCAATGATTGAGAAATACCTTGTGTGCC 584
Db 541 AGCCATGCCCATGCGCAATGATTGAGAAATACCTTGTGTGCC 584

RESULT 3
ID AAA28724 standard; DNA; 1686 BP.
AC AAA28724;
XX 29-AUG-2000 (first entry)
XX Human osteoprotegrin-like 1 (OPGx1) DNA.

XX OPGx1; osteoprotegrin-like; DR6 TNF-related death receptor; agonist;
KW inhibitor; bone resorption; vascular calcification; apoptosis;
KW osteopathic; chromosome 6p11.1; D6S452; ss.
XX Homo sapiens.
XX Key Location/Qualifiers
FT CDS 102..974
FT FT /*tag= a
FT FT /product= "OPGx1"
XX WO200024771-A2.
XX 04-MAY-2000.
XX 22-OCT-1999; 99WO-US024913.
XX 23-OCT-1998; 98US-0105481P.
XX 01-OCT-1999; 99US-0156993P.
XX 21-OCT-1999; 99US-00422680.
XX (CURA-) CURAGEN CORP.

XX Shimkets RA, Yang M, Lichenstein H, McDonald WF;
XX WPI; 2000-350692/30.
XX P-PSDB; AAY92842.

XX Nucleic acids encoding osteoprotegrin-like (OPGx) polypeptides, useful
XX for treating disorders associated with bone metabolism, such as
XX osteoporosis and osteopetrosis.

XX Claim 1; Fig 1; 81pp; English.
XX Osteoprotegrin-like polypeptides (OPGx) are expressed in bone, lymph
XX node, germinal B cells and kidney. There appear to be at least two splice
XX variants of this gene, a transmembrane form and an extracellular domain
XX form. Human OPGx1, 2 and 4 contain a 36 amino acid extension at their N-

CC terminal relative to the DR6 tumour necrosis factor (TNF)-related death
CC receptor. The OPGx gene has been mapped to chromosome 6p11.1, essentially
CC on top of D6S452. The OPGx polypeptides, agonists and antibodies are
CC useful in methods to inhibit osteoclast-mediated bone resorption or
CC vascular calcification and to modulate cell death (apoptosis). This is
CC useful for treating disorders associated with bone metabolism, such as
CC osteoporosis, osteopetrosis, or a condition characterized by loss of
CC bone, breakdown of tissue, or excessive resorption of bone tissue
XX SQ Sequence 1686 BP; 438 A; 429 C; 408 G; 406 T; 0 U; 5 Other;

Query Match 97.9%; Score 571.6; DB 3; Length 1686;
Best Local Similarity 99.1%; Pred. No. 5e-124;
Matches 579; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GCGNCCGCGNNGNCAAGGTGCTCAGCGCCCTAGNCGCTCCCTTGGCGCTCCCTCC 60
Db 1 GCGNCCGCGNNGNCAAGGTGCTCAGCGCCCTAGNCGCTCCCTTGGCGCTCCCTCC 60
Qy 61 TCTGCGCGCGCTGAGTGCATGCGGGTGTGGAGGTAGATGGGCTCCCGCGCGGAG 120
Db 61 TCTGCGCGCGCTGAGTGCATGCGGGTGTGGAGGTAGATGGGCTCCCGCGCGGAG 120
Qy 121 GCGCGGTGATGCGCGGCTGGGCAAGAGCGCGCGATTTCCAGCTGCCCGCGCGCC 180
Db 121 GCGCGGTGATGCGCGGCTGGGCAAGAGCGCGCGATTTCCAGCTGCCCGCGCGCC 180
Qy 181 CGGCCACCTTGGAGTCCCGGTTTCCAGCATGGGACCTCTCCGAGCAGCAGCAGCCG 240
Db 181 CGGCCACCTTGGAGTCCCGGTTTCCAGCATGGGACCTCTCCGAGCAGCAGCAGCCG 240
Qy 241 TCGCCTCTCTGAGCGCATCGCCGCGAGCCACAGCAGCATGATCGCGGCTCCCTTC 300
Db 241 TCGCCTCTCTGAGCGCATCGCCGCGAGCCACAGCAGCATGATCGCGGCTCCCTTC 300
Qy 301 TCTGCTTGGATTCTTTAGCACCACAGCAGTCCAGCAGCAGCAGCAGCAGCAGTCA 360
Db 301 TCTGCTTGGATTCTTTAGCACCACAGCAGTCCAGCAGCAGCAGCAGCAGCAGTCA 360
Qy 361 TTGGCACAATACCGCATGTTGACCGTGCCACCGCGCGAGTGAACCTGTGACAAGTGT 420
Db 361 TTGGCACAATACCGCATGTTGACCGTGCCACCGCGCGAGTGAACCTGTGACAAGTGT 420
Qy 421 CAGCAGAACTATGCTCTGAGCATGTATACCAACAGCCGCTGCGGCTGAGCAGATT 480
Db 421 CAGCAGAACTATGCTCTGAGCATGTATACCAACAGCCGCTGCGGCTGAGCAGATT 480
Qy 481 GCCTGTGGGGACCTTTACCAAGCATGAGAAATACCTTGTGTGCC 540
Db 481 GCCTGTGGGGACCTTTACCAAGCATGAGAAATACCTTGTGTGCC 540
Qy 541 AGCCATGCCCATGCGCAATGATTGAGAAATACCTTGTGTGCC 584
Db 541 AGCCATGCCCATGCGCAATGATTGAGAAATACCTTGTGTGCC 584

RESULT 4
ID AAA28726 standard; DNA; 1686 BP.
XX AAA28726;
XX 29-AUG-2000 (first entry)
XX Human osteoprotegrin-like 4 (OPGx4) DNA.

XX OPGx4; osteoprotegrin-like; DR6 TNF-related death receptor; agonist;
KW inhibitor; bone resorption; vascular calcification; apoptosis;
KW osteopathic; chromosome 6p11.1; D6S452; ss.
XX Homo sapiens.
XX Key Location/Qualifiers

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FT CDS 102..974
FT /*tag= a
FT /product= "OPGx4"
XX PN WO200024771-A2.
XX PD 04-MAY-2000.
XX PF 22-OCT-1999; 99WO-US024913.
XX PR 23-OCT-1998; 98US-0105481P.
XX PR 01-OCT-1999; 99US-0156993P.
XX PR 21-OCT-1999; 99US-00422680.
XX PA (CURA-) CURAGEN CORP.
XX PI Shimkets RA, Yang M, Lichenstein H, Mcdonald WF;
XX P-PSDB; AAY92844.
XX DR Nucleic acids encoding osteoprotegerin-like (OPGx) polypeptides, useful
XX for treating disorders associated with bone metabolism, such as
XX osteoporosis and osteopetrosis.
XX PS Claim 1; Fig 6; 81pp; English.
XX CC Osteoprotegerin-like polypeptides (OPGx) are expressed in bone, lymph
CC node, germinal B cells and kidney. There appear to be at least two splice
CC variants of this gene, a transmembrane form and an extracellular domain
CC form. Human OPGx1, 2 and 4 contain a 36 amino acid extension at their N-
CC terminal relative to the DR6 tumour necrosis factor (TNF)-related death
CC receptor. The OPGx gene has been mapped to chromosome 1p11.1, essentially
CC on top of D6S452. The OPGx polypeptides, agonists and antibodies are
CC useful in methods to inhibit osteoclast-mediated bone resorption or
CC vascular calcification and to modulate cell death (apoptosis). This is
CC useful for treating disorders associated with bone metabolism, such as
CC osteoporosis, osteopetrosis, or a condition characterized by loss of
CC bone, breakdown of tissue, or excessive readorption of bone tissue
XX SQ Sequence 1686 BP; 435 A; 428 C; 406 G; 410 T; 0 U; 7 Other;

Query Match 97.6%; Score 570; DB 3; Length 1686;
Best Local Similarity 99.0%; Pred. No. 1.2e-123;
Matches 578; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GCGNCCGCGNNGNGCAAGGTGCTGAGCGCCCTAGNGCCTCCTTTCGCGCTCCCTCC 60
DB 1 GCGNCCGCGNNGNGCAAGGTGCTGAGCGCCCTAGAGCCTCCTTTCGCGCTCCCTCC 60
QY 61 TCTGCCCGCGGTAGCAGTGCACATGGGGTGTGGAGGTAGTGGGCTCCCGCGCGGAG 120
DB 61 TCTGCCCGCGGTAGCAGTGCACATGGGGTGTGGAGGTAGTGGGCTCCCGCGCGGAG 120
QY 121 GCGGCGGTGATGCGGCGCTGGGCGAGAGCAGCGCCGATTCAGCTGCCCGCGCGGCC 180
DB 121 GCGGCGGTGATGCGGCGCTGGGCGAGAGCAGCGCCGATTCAGCTGCCCGCGCGGCC 180
QY 181 GCGGCACCTTCGAGTCCCGGTTTCAGCCATGGGGACCTTCGAGCAGCAGCAGCC 240
DB 181 GCGGCACCTTCGAGTCCCGGTTTCAGCCATGGGGACCTTCGAGCAGCAGCAGCAGC 240
QY 241 TCGCCTCTCAGCGCATGCCCGCGAGCCACAGCCAGCATGATCGCGGGCTCCCTTC 300
DB 241 TCGCCTCTCAGCGCATGCCCGCGAGCCACAGCCAGCATGATGATCGCGGGCTCCCTTC 300
QY 301 TCCTGCTTGGATTCCTTAGCACCACACAGCTCAGCCAGAACAGAGGCTCGAATCTCA 360
DB 301 TCCTGCTTGGATTCCTTAGCACCACACAGCTCAGCCAGAACAGAGGCTCGAATCTCA 360
QY 361 TTGGCACAATACCGCATTTGACCGTGCACCGCCAGGTGCTTAACCTGACAGAGTGC 420
DB 361 TTGGCACAATACCGCATTTGACCGTGCACCGCCAGGTGCTTAACCTGACAGAGTGC 420

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421 CAGCAGGAACCTATGTCTCTGAGCATTTGTACCAACACAGCTGGCGTCTGACAGTT 480

421 CAGCAGGAACCTATGTCTCTGAGCATTTGTACCAACACAGCTGGCGTCTGACAGTT 480

481 GCCCTGTGGGACCTTTTACCAGGCATGAGAAATGGCATAGAGAAATGCCATGACTAGTC 540

481 GCCCTGTGGGACCTTTTACCAGGCATGAGAAATGGCATAGAGAAATGCCATGACTAGTC 540

541 AGCCATGCCCATGGCCAAATGATTGAGAAATTACCTTGTGCTGCC 584

541 AGCCATGCCCATGGCCAAATGATTGAGAAATTACCTTGTGCTGCC 584

RESULT 5

AA25260

ID AAX25260 standard; cDNA; 2646 BP.

XX AC AAX25260;

XX DT 19-JUL-1999 (first entry)

XX DE Human soluble tumour necrosis factor receptor ZTNFR-6 cDNA.

XX KW ZTNFR-6; tumour necrosis factor receptor-6; human; cell maturation;

XX KW bone cell regulation; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX CDS 284..973

XX FT /*tag= a

XX FT /product= "soluble ZTNFR-6"

XX FT /note= "this region of the sequence is specifically

XX FT claimed in Claim 10(b)"

XX FT 284..334

XX FT sig_peptide /*tag= b

XX FT 335..973

XX FT mat_peptide /*tag= c

XX WO9911790-A1.

XX 11-MAR-1999.

XX 03-SEP-1998; 98WO-US018364.

XX 04-SEP-1997; 97US-0057608P.

XX 04-SEP-1997; 97US-00923725.

XX (ZYMO) ZYMOGENETICS INC.

XX Farrah TM, Gross JA, Matthews SM;

XX WPI; 1999-205190/17.

XX P-PSDB; AAY05679.

XX New secreted or membrane bound tumor necrosis factor receptor ZTNFR-6 -

XX useful for detecting a genetic abnormality in a patient.

XX Claim 11a; Page 115-117; 145pp; English.

XX This is the DNA sequence of an isolated polynucleotide that codes for a

XX novel human soluble tumour necrosis factor receptor, designated ZTNFR-6

XX (see AAY05679). The polynucleotide was initially identified by querying

XX an EST database for sequences homologous to conserved motifs within the

XX TNFR family. A second clone (see AAX25279) encodes a membrane-bound ZTNFR

XX -6 (see AAY05678); it includes a 40 bp exon (see AAX25262) that puts the

XX sequence in frame for the transmembrane and cytoplasmic domains of

XX membrane-bound ZTNFR-6. The human ZTNFR-6 gene was localised to 6p21.1.

XX The isolated polynucleotides can be utilised in the recombinant

XX production of ZTNFR-6 polypeptides, and also in a claimed method for

XX detecting a genetic abnormality in a patient. ZTNFR-6 polypeptides are

XX useful in methods that promote cellular maturation and bone cell

CC	regulation	XX	Sequence	2646 BP;	664 A;	722 C;	666 G;	594 T;	0 U;	0 Other;
Query	Match		93.6%;	Score	546.4;	DB	2;	Length	2646;	
Best	Local		Similarity	97.6%;	Pred.	No.	4.2e-118;			
Matches	572;	Conservative	0;	Mismatches	12;	Indels	2;	Gaps	2;	
Qy	1	GC	GC	GC	GC	GC	GC	GC	GC	GC
Db	1	GC	GC	GC	GC	GC	GC	GC	GC	GC
Qy	61	TC	TC	TC	TC	TC	TC	TC	TC	TC
Db	61	TC	TC	TC	TC	TC	TC	TC	TC	TC
Qy	120	GC	GC	GC	GC	GC	GC	GC	GC	GC
Db	121	GC	GC	GC	GC	GC	GC	GC	GC	GC
Qy	180	CC	-GGC	CAC	CTT	GG	AGT	CC	CGG	CT
Db	181	CC	GG	CG	CC	CT	GG	AGT	CC	CGG
Qy	239	CT	TC	CG	CT	TC	TC	TC	TC	TC
Db	241	CT	TC	CG	CT	TC	TC	TC	TC	TC
Qy	299	TC	TC	TC	TC	TC	TC	TC	TC	TC
Db	301	TC	TC	TC	TC	TC	TC	TC	TC	TC
Qy	359	CAT	TGG	CAC	ATA	CC	CG	CAT	TT	GAC
Db	361	CAT	TGG	CAC	ATA	CC	CG	CAT	TT	GAC
Qy	419	TC	CAG	CAG	GA	AC	CT	AT	TT	GAC
Db	421	TC	CAG	CAG	GA	AC	CT	AT	TT	GAC
Qy	479	TT	GC	CT	GT	GG	GA	AC	CT	TT
Db	481	TT	GC	CT	GT	GG	GA	AC	CT	TT
Qy	539	TC	AG	CC	AT	TG	GC	CA	AT	TG
Db	541	TC	AG	CC	AT	TG	GC	CA	AT	TG

RESULT 6	
AAAX25261	
ID	AAAX25261 standard; cDNA; 2696 BP.
XX	
XX	
AC	AAAX25261;
AC	
XX	
XX	
DT	19-JUL-1999 (first entry)
DT	
XX	
DE	Tumour necrosis factor receptor ZTNFR-6 cDNA (incorrectly spliced).
XX	
XX	
KW	ZTNFR-6; tumour necrosis factor receptor-6; human; cell maturation;
KW	bone cell regulation; ss.

PH	Key	Location/Qualifiers
FT	CDS	284..1810
FT		/*tag= a
XX		
XX	WO9911790-A1.	
XX		
XX	11-MAR-1999.	
XX		
XX	03-SEP-1998;	
PF		98WO-US018364.

XX	04-SEP-1997;	97US-0057608P.	
PR	04-SEP-1997;	97US-0092372S.	
XX			
PA	(ZYMO) ZYMOGENETICS INC.		
XX			
PI	Farrah TM, Gross JA, Matthews SM;		
XX			
DR	WFI; 1999-205190/17.		
DR	P-PSDB; AAY05680.		
XX			
PT	New secreted or membrane bound tumor necrosis factor receptor ZTNFR-6 -		
PT	useful for detecting a genetic abnormality in a patient.		
XX			
PS	Disclosure; Page 103-107; 145pp; English.		
XX			
CC	This novel 2686 bp DNA sequence has homology to members of the tumour		
CC	necrosis factor receptor (TNFR) family, and is designated ZTNFR-6.		
CC	Analysis of the sequence indicated that the C-terminal portion following		
CC	the death domain of ZTNFR-6 was incorrectly spliced. A claimed, correctly		
CC	spliced sequence is given AAX25259. ZTNFR-6 polypeptides are useful in		
CC	methods that promote cellular maturation and bone cell regulation		
XX			
SQ	Sequence 2686 BP; 675 A; 734 C; 672 G; 605 T; 0 U; 0 Other;		
	Query Match	93.6%; Score 546.4; DB 2; Length 2686;	
	Best Local Similarity	97.6%; Pred. No. 4.2e-118;	
	Matches	572; Conservative 0; Mismatches 12; Indels 2; Gaps 2;	
Qy	1	GCNCGCCGNGNGNCAGGTCGTAGCGCCCTCCTAGNGCCTCCCTTGCCTCCTCCCTCC 60	
Db	1	GCGCCCGCGCGCTCGGCGAGTGCTGAGCGCCCTAGAGCCTCCCTTGCCTCCTCCCTCC 60	
Qy	61	TCCTGCCCGCGCTAGCAGTGCACATGGGGTGTGGAGGTAGATGGGCTCCCGG-CGGGA 119	
Db	61	TCCTGCCCGCGCTAGCAGTGCACATGGGGTGTGGAGGTAGATGGGCTCCCGGCCGGGA 120	
Qy	120	GGCGGGGCTGGATGCGGCGCTGGGCGAGAGCAGCCGCGGATTCAGCTGCCCGCGGCC 179	
Db	121	GGCGGGGCTGGATGCGGCGCTGGGCGAGAGCAGCCGCGGATTCAGCTGCCCGCGGCC 180	
Qy	180	CC-GGCCACCTTCGGAGTCCCGGTTTCAGCCATGGGGACCTCTCCGAGCAGCAGCACCG 238	
Db	181	CCGGCGCCCTTCGGAGTCCCGGTTTCAGCCATGGGGACCTCTCCGAGCAGCAGCACCG 240	
Qy	239	CCTCGCTCTCTGAGCCGCGATCCCGCGCGAGCCACAGCCAGATGATCGGGCTCCCT 298	
Db	241	CCTCGCTCTCTGAGCCGCGATCCCGCGCGAGCCACAGCCAGATGATCGGGCTCCCT 300	
Qy	299	TCCTCTGCTTGGATTCCTTAGCACCCACACAGCTCAGCCAGACAGAGGCTCGATCT 358	
Db	301	TCCTCTGCTTGGATTCCTTAGCACCCACACAGCTCAGCCAGACAGAGGCTCGAATCT 360	
Qy	359	CATTGGCACATACCGCCATGTTGACCGTGCACCGCGCAGGTGCTAACCTGTGACAAAGT 418	
Db	361	CATTGGCACATACCGCCATGTTGACCGTGCACCGCGCAGGTGCTAACCTGTGACAAAGT 420	
Qy	419	TCAGCAGGAACCTATGTCTCTGAGCATTGTATCAACACAAAGCCTGGCGCTGTGCAGCAG 478	
Db	421	TCCAGCAGGAACCTATGTCTCTGAGCATTGTATCAACACAAAGCCTGGCGCTGTGCAGCAG 480	
Qy	479	TTGCCCTGTGGGACCTTTTACCAGGATGAGATGGCATAGAGAAATGCCATGACTGTAG 538	
Db	481	TTGCCCTGTGGGACCTTTTACCAGGATGAGATGGCATAGAGAAATGCCATGACTGTAG 540	
Qy	539	TCAGCCATGCCCATGGCCAAATGATTGAGAAATACCTTGTGTGCTGCC 584	
Db	541	TCAGCCATGCCCATGGCCAAATGATTGAGAAATACCTTGTGTGCTGCC 586	

RESULT 7
AAX25259
ID AAX25259 standard; cDNA; 3440 BP.

XX AAX25259;
 AC
 XX
 DT 19-JUL-1999 (first entry)
 XX
 DE Human full-length tumour necrosis factor receptor ZTNFR-6 cDNA.
 XX
 KW ZTNFR-6; tumour necrosis factor receptor-6; human; cell maturation;
 XX bone cell regulation; ss.
 OS Homo sapiens.
 XX
 XX
 FH Key Location/Qualifiers
 FT misc_feature 284..2225
 FT /tag= b
 FT /note= "this region of the sequence is specifically
 FT claimed in Claim 10(a)"
 FT CDS 284..2179
 FT /tag= a
 FT /product= "membrane-bound ZTNFR-6"
 FT sig_peptide 284..334
 FT /tag= c
 FT mat_peptide 335..2176
 FT /tag= d
 FT
 XX WO9911790-A1.
 XX
 XX 11-MAR-1999.
 PD
 XX
 XX 03-SEP-1998; 98WO-US018364.
 XX
 XX 04-SEP-1997; 97US-0057608P.
 PR
 XX 04-SEP-1997; 97US-00923725.
 PR
 XX
 XX (ZYMO) ZYMOGENETICS INC.
 PA
 XX Farrah TM, Gross JA, Matthews SM;
 PI
 XX WPI; 1999-205190/17.
 DR
 XX P-PSDB; AAY05678.
 DR
 XX
 XX New secreted or membrane bound tumor necrosis factor receptor ZTNFR-6 -
 PT useful for detecting a genetic abnormality in a patient.
 PT
 XX
 XX Claim 10a; Page 108-113; 145pp; English.
 PS
 XX
 CC This is the DNA sequence of an isolated polynucleotide that codes for a
 CC novel human full-length membrane-bound tumour necrosis factor receptor,
 CC designated ZTNFR-6 (see AAY05678). The polynucleotide was initially
 CC identified by querying an EST database for sequences homologous to
 CC conserved motifs within the TNFR family. A second clone (see AAX25260)
 CC encodes truncated, soluble ZTNFR-6 (see AAY05679). The full-length clone
 CC includes a 40 bp exon (see AAX25262) that puts the sequence in frame for
 CC the transmembrane and cytoplasmic domains of membrane-bound ZTNFR-6. The
 CC human ZTNFR-6 gene was localised to 6p21.1. The isolated polynucleotides
 CC can be utilised in the recombinant production of ZTNFR-6 polypeptides,
 CC and also in a claimed method for detecting a genetic abnormality in a
 CC patient. ZTNFR-6 polypeptides are useful in methods that promote cellular
 CC maturation and bone cell regulation
 CC
 XX
 SQ Sequence 3440 BP; 827 A; 876 C; 833 G; 904 T; 0 U; 0 Other;
 Query Match 93.68; Score 546.4; DB 2; Length 3440;
 Best Local Similarity 97.67; Pred. No. 4.4e-118;
 Matches 572; Conservative 0; Mismatches 12; Indels 2; Gaps 2;
 QY 1 GCGGCCCGGNGNGCAAGTGCTGAGCGCCCTAGNGCTCCCTTGGCGCTCCCTCC 60
 DB 1 GCGGCCCGCGCTGGCGAGGTGCTGAGCGCCCTAGAGCTCCCTTGGCGCTCCCTCC 60
 QY 61 TCTGCCCGCGCTAGCAGTGACATGGGGTGTTCGAGGTAGATGGGCTCCCGG-CCGGGA 119
 DB 61 TCTGCCCGCGCTAGCAGTGACATGGGGTGTTCGAGGTAGATGGGCTCCCGCGCGGGA 120

QY 120 GCGCGCGTGGATGCGGCGCTGGGAGAGCAGCGCGGATTCCAGCTGCCCGCGCGCC 179
 DB 121 GCGCGCGTGGATGCGGCGCTGGGAGAGCAGCGCGGATTCCAGCTGCCCGCGCGCC 180
 QY 180 CC-GGCCACCTTTGCGAGTCCCGGGTTCCAGCCATGGGACCTCTCCGAGCAGCAGCACCGC 238
 DB 181 CGGGCGCGCTTGGAGTCCCGGGTTCCAGCCATGGGACCTCTCCGAGCAGCAGCACCGC 240
 QY 239 CCTCGCTCTTGGAGCAGCGCATGCGCGCGGAGCAGCAGCAGCAGTATCGGGGCTCCCT 298
 DB 241 CCTCGCTCTTGGAGCAGCGCATGCGCGCGGAGCAGCAGCAGCAGTATCGGGGCTCCCT 300
 QY 299 TCTCTGCTTGGATTCTTAGCACCACACAGCTCAGCCAGAACAGAGGCTCCGAATCT 358
 DB 301 TCTCTGCTTGGATTCTTAGCACCACACAGCTCAGCCAGAACAGAGGCTCCGAATCT 360
 QY 359 CATTTGGCACATACCGCCATGTTGACCGTGCCACCGCCAGGTGCTTAACCTGTGACAAGTG 418
 DB 361 CATTTGGCACATACCGCCATGTTGACCGTGCCACCGCCAGGTGCTTAACCTGTGACAAGTG 420
 QY 419 TCCAGCAGAACCTATGTCTCTGAGCATTTACCAACAAGCCCTGCGGCTTGAGCAGCAG 478
 DB 421 TCCAGCAGAACCTATGTCTCTGAGCATTTACCAACAAGCCCTGCGGCTTGAGCAGCAG 480
 QY 479 TTGCGCTTGGGGACCTTTACCAGCATGAGAAATGGCATAGAGAAATGCCATGACTGTAG 538
 DB 481 TTGCGCTTGGGGACCTTTACCAGCATGAGAAATGGCATAGAGAAATGCCATGACTGTAG 540
 QY 539 TCAGCCATGCCCATGCCCAATGATTGAGAAATTTACCTTTGTGTGCC 584
 DB 541 TCAGCCATGCCCATGCCCAATGATTGAGAAATTTACCTTTGTGTGCC 586

RESULT 8

AAH14374
 ID AAH14374 standard; cDNA; 2636 BP.
 XX
 AC AAH14374;
 XX
 DT 26-JUN-2001 (first entry)
 XX
 DE Human cDNA sequence SEQ ID NO:11786.
 XX
 KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
 XX
 OS Homo sapiens.
 XX
 PN EP1074617-A2.
 XX
 PD 07-FEB-2001.
 XX
 PF 28-JUL-2000; 2000EP-00116126.
 XX
 PR 29-JUL-1999; 99JP-00248036.
 PR 27-AUG-1999; 99JP-00300253.
 PR 11-JAN-2000; 2000JP-00118776.
 PR 02-MAY-2000; 2000JP-00183767.
 PR 09-JUN-2000; 2000JP-00241899.
 XX
 XX (HELI-) HELIX RES INST.

XX
 XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Teshi S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 XX
 DR WPI; 2001-318749/34.
 XX

XX Primer sets for synthesizing polynucleotides, particularly the 5602 full-
 PT length cDNAs defined in the specification, and for the detection and/or
 PT diagnosis of the abnormality of the proteins encoded by the full-length
 PT cDNAs.

XX Claim 8; SEQ ID NO 11786; 2537pp + Sequence Listing; English.
 PS

XX The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention

XX Sequence 2636 BP; 569 A; 762 C; 722 G; 583 T; 0 U; 0 Other;

Query Match		93.3%;	Score 544.8;	DB 4;	Length 2636;
Best Local Similarity		97.4%;	Pred. No. 1e-117;		
Matches 571;		Conservative 0;	Mismatches 13;	Indels 2;	Gaps 2;
QY	1	GCNCCGCGNNGNCAGGTGCTGAGCGCCCTAGNGCCTCCCTTGGCGCTCCCTCC	60		
Db	184	GCGCGCGCGCGCTGGGAGGTGCTGAGCGCCCTAGAGCCTCCCTTGGCGCTCCCTCC	243		
QY	61	TCTGCCGCGCGTAGACATGACATGGGTGTGGAGGTAGATGGGTCCCGG-CGGGGA	119		
Db	244	TCTGCCGCGCGCGTAGACATGACATGGGTGTGGAGGTAGATGGGTCCCGGCGCGGGA	303		
QY	120	GCGCGCGGTGGATGCGCGCTGGGAGAGCAGCAGCCGATCCAGCTGCCCGCGCGCC	179		
Db	304	GCGCGCGGTGGATGCGCGCTGGGAGAGCAGCAGCCGATCCAGCTGCCCGCGCGCC	363		
QY	180	CC-GGCGACCTTGGAGTCCCGGTTTCAGCCATGGGACCTCTCCGAGCAGCAGCACCGC	238		
Db	364	CCGCGCGCCCTTGGAGTCCCGGTTTCAGCCATGGGACCTCTCCGAGCAGCAGCACCGC	423		
QY	239	CCTCGGCTCTCGAGCGCGATCGCGCGCCGAGCCACAGCCACGATGATCGCGGCTCCCT	298		
Db	424	CCTCGGCTCTCGAGCGCGATCGCGCGCCGAGCCACAGCCACGATGATCGCGGCTCCCT	483		
QY	299	TCTCCTGCTGGATTCCTTAGCACCACACAGCTCAGCCAGACAGAGGCTCGAATCT	358		
Db	484	TCTCCTGCTGGATTCCTTAGCACCACACAGCTCAGCCAGACAGAGGCTCGAATCT	543		
QY	359	CATTGGCACATACCGCATGTCACCTGTCACCGGCGAGGTCTAACCTGTGACAAAGTG	418		
Db	544	CATTGGCACATACCGCATGTCACCTGTCACCGGCGAGGTCTAACCTGTGACAAAGTG	603		
QY	419	TCAGCAGGAACTATGCTCTGAGCATTTGTACCAACAAAGCTCGCGCTCTGCAGCAG	478		
Db	604	TCCAGCAGGAACTATGCTCTGAGCATTTGTACCAACAAAGCTCGCGCTCTGCAGCAG	663		
QY	479	TTGCGCTGTGGGACCTTTTACCAGGCATGAGATGGCATGAGAAATGCCATGCTGTAG	538		
Db	664	TTGCGCTGTGGGACCTTTTACCAGGCATGAGATGGCATGAGAAATGCCATGCTGTAG	723		
QY	539	TCAGCATGCGCATGGCAATGATTGAGAAATACCTTTGCTGCC	584		
Db	724	TCAGCATGCGCATGGCAATGATTGAGAAATACCTTTGCTGCC	769		

ID	AAX25322 standard; cDNA; 2638 BP.
XX	
AC	AAX25322;
XX	
DT	19-JUL-1999 (first entry)
XX	
DE	Human TNF receptor TRL II cDNA.
XX	
KW	TRL II; TNF receptor-like; tumour necrosis factor receptor; human; signal transduction; cell differentiation; prostate cancer; inflammation; arthritis; diabetes; insulin resistance; diagnosis; therapy; ss.
KW	
XX	Homo sapiens.
OS	
Key	Location/Qualifiers
FT	510..2327
CDS	/*tag= a
FT	sig_peptide
FT	510..632
FT	/*tag= b
FT	mat_peptide
XX	633..2324
PN	WO9915663-A1.
XX	
PD	01-APR-1999.
XX	
PF	25-SRP-1998; 98WO-US020219.
XX	
PR	26-SEP-1997; 97US-00938896.
PR	17-MAR-1998; 98US-00042785.
XX	
PA	(MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
XX	
PI	Busfield SJ;
XX	
DR	WPI; 1999-254712/21.
XX	P-PSDB; AAY05697.
PT	Nucleic acid encoding tumor necrosis factor receptor-like protein.
XX	
PS	Claim 1b; Page 148-153; 170pp; English.
XX	
CC	This cDNA sequence codes for a novel member of the human tumour necrosis factor receptor superfamily (see AAY05697), termed TRL II (TNF receptor-like). A plasmid containing the full-length nucleotide sequence encoding human TRL II (clone eph75L) is deposited as ATCC 98649. TRL II has a mol.wt. of 66.2 kDa. It is a membrane-bound protein that has 4 cysteine-rich domains and a C-terminal death domain (see AAY05698). TRL II cDNA was isolated from a HeLa cDNA library using mouse TRL cDNA (see AAX25320) as probe. An alternatively spliced, secreted form, human TRL I (see AAX25321), has also been identified. Chromosomal mapping located the TRL gene on chromosome 6p25. The invention provides full-length TRL proteins, TRL fusion proteins, antigenic peptides and anti-TRL antibodies, as well as TRL nucleic acids, recombinant expression vectors, host cells and non-human transgenic animals. TRL are regulators or modulators of cellular signal transduction, cellular proliferation or differentiation, cell survival and apoptosis, immune system cells, and cells involved in insulin resistance or the diabetic response. They can be used to isolate cognate ligands, to modulate ligand/TRL interactions, to screen for potential modulators, and to treat conditions associated with abnormal TRL levels. TRL nucleic acids are used for recombinant production of TRL, to detect mutations, to identify TRL homologues, as antisense, triplex-forming or ribozyme therapeutics, for chromosome mapping and for forensic identification of individuals. Antibodies, antisense sequences, TRL protein mutants etc. that modulate activity of TRL are used to treat or prevent conditions associated with aberrant TRL protein or expression, e.g. cell proliferation and differentiation disorders (particularly cancer, especially of the prostate), inflammation (e.g. arthritis) and metabolic disease (e.g. diabetes and insulin resistance)
XX	
QQ	Sequence 2638 BP; 625 A; 749 C; 701 G; 563 T; 0 U; 0 Other;

Best Local Similarity 97.4%; Pred. No. 1e-117;
Matches 571; Conservative 0; Mismatches 13; Indels 2; Gaps 2;
QY 1 GCGNCCGCGNNGNGCAAGGTCTGAGCGCCCTAGNGCCTCCCTTGGCGCTCCCTCC 60
Db 299 GCGCGCGCGCGCTGGCGAGTGTCTGAGCGCCCTAGAGCCTCCCTTGGCGCTCCCTCC 358
QY 61 TCTGCCCGCGCTAGCAGTGCACATGGGGTGTGGAGGTAGATGGGCTCCCGG-CCGGGA 119
Db 359 TCTGCCCGCGCGCAGCAGTGCACATGGGGTGTGGAGGTAGATGGGCTCCCGGCGGGA 418
QY 120 GCGCGCGGTGGATGCGCGCTGGGCGAGCAGCAGCCCGGATTCAGTGTGCGCGCGCC 179
Db 419 GCGCGCGGTGGATGCGCGCTGGGCGAGCAGCAGCCCGGATTCAGTGTGCGCGCGCC 478
QY 180 CC-GGCCACCTTCGAGTCCCGGTTCCAGCATGGGGACCTCCGAGCAGCAGCACCGC 238
Db 479 CCGGCGCGCCCTCGAGTCCCGGTTCCAGCATGGGGACCTCCGAGCAGCAGCACCGC 538
QY 239 CTTGCGCTCTCTGAGCGCGCATCGCCGCGAGCAGCAGCAGCATGATCGCGGCTCCCT 298
Db 539 CTTGCGCTCTCTGAGCGCGCATCGCCGCGAGCAGCAGCAGCATGATCGCGGCTCCCT 598
QY 299 TCTCTGCTTGGATCTTAGCACCACAGCTCAGCCAGAACAGAGGCTTCGAATCT 358
Db 599 TCTCTGCTTGGATCTTAGCACCACAGCTCAGCCAGAACAGAGGCTTCGAATCT 658
QY 359 CATGSCACATACCGGCATGTTGACCGTGCACCGCCAGGTGCTAACCTGTGACAGTG 418
Db 659 CATGSCACATACCGGCATGTTGACCGTGCACCGCCAGGTGCTAACCTGTGACAGTG 718
QY 419 TCAGCAGGAACCTATGCTCTGAGCATTTGACCAACAGCGCTGCGGCTCTGACGACG 478
Db 719 TCAGCAGGAACCTATGCTCTGAGCATTTGACCAACAGCGCTGCGGCTCTGACGACG 778
QY 479 TTGCGCTGTGGGACCTTTACAGGATGAGATGAGATGAGAAATGCGATGCTGTAG 538
Db 779 TTGCGCTGTGGGACCTTTACAGGATGAGATGAGATGAGAAATGCGATGCTGTAG 838
QY 539 TCAGCAGCATCCCATGCCAATGATTGAGAAATACCTTGTGCTGCC 584
Db 839 TCAGCAGCATCCCATGCCAATGATTGAGAAATACCTTGTGCTGCC 884
AAZ92406
ID AAZ92406 standard; cDNA; 2877 BP.
XX
AC AAZ92406;
DT
DT 05-JUN-2000 (first entry)
XX
DE cDNA encoding human TNF receptor-like protein HSLJD37R, SEQ ID NO:9.
XX
XX TNF receptor family; tumour necrosis factor; HDTEA84; HSLJD37R;
KW Rank-like protein; RANKL; immune disorder; inflammation; allergy;
KW immunosuppressant; antiarthritic; antirheumatoid; antiinflammatory;
KW dermatological; antithyroid; ss.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FT 410..2377
CDS /*tag= a
ET /product= "Human HSLJD37R"
FT
XX
PN WO20001817-A2.
XX
XX 13-JAN-2000.
XX
XX 06-JUL-1999; 99WO-US012366.
PF
XX
XX 06-JUL-1998; 98US-00110938.
PR

PR 13-JUL-1998; 98US-00114466.
PR 23-JUL-1998; 98US-0093897P.
PR 12-AUG-1998; 98US-0013296P.
PR 18-AUG-1998; 98US-00136214.
PR 11-SEP-1998; 98US-0099999P.
XX
PA (SCHE) SCHERING CORP.
XX
XX Bates BM, Lebecque SJE, Murphy EE, Mattson JD, Gorman DM;
PI Hedrick JA, Wang L, Zlotnik A, Murgolo NJ, Greene JR, Johnston JA;
PI Bazan JF, Mahony D, Lees EM;
XX
XX WPI; 2000-171015/15.
DR P-PSDB; AAV77460.
XX
PT New isolated mammalian genes, used to develop products for treating e.g.
PT immune, inflammatory or allergic abnormalities, cancers or degenerative
PT conditions.
XX
PS Claim 25; Page 160-163; 218pp; English.
XX
CC The invention relates to a number of primate and/or rodent proteins, and
CC the genes which encode them. The invention encompasses human dendritic
CC cell prostaglandin transporter (DC-PGT); the TNF (tumour necrosis factor)
CC receptor family-related proteins HDTEA84, HSLJD37R and RANKL; human CC
CC chemokine HCC5; human deubiquitinating proteins Dub11 and Dub 12; human
CC MD-1 and human and murine MD-2 proteins, which exhibit the properties of
CC ligands for proteins comprising a leucine-rich motif (LRR); human cyclin
CC E2; cDNAs encoding these proteins; and antibodies against these proteins.
CC The proteins can be used for modulating the physiology or development of
CC a cell. They can be used to mediate uptake of substrates (e.g.,
CC prostaglandin-like molecules), to modulate or mediate cellular
CC interactions (e.g., induce or prevent trafficking, proliferation, or
CC differentiation of cells), or are intracellular proteins which are
CC important in various cellular processes such as the deubiquitination of
CC proteins or cell cycle regulation. The products can be used for treating
CC medical conditions such as immune, inflammatory or allergic disorders, or
CC abnormal cellular proliferation, for example, cancers or degenerative
CC conditions. They can be used to modulate immune responses in disease
CC states e.g., autoimmune disorders, including rheumatoid arthritis, as well
CC as systemic lupus erythematosus, Hashimoto's autoimmune thyroiditis, as well
CC as acute and chronic inflammatory responses in which T cell activation,
CC expansion, and/or immunological T cell memory play an important role.
CC Sequences AAZ92404-292411 represent cDNAs encoding TNF receptor family-
CC related proteins. AAZ92404 encodes the human protein HDTEA84, AAZ92405-
CC 292407 encode human HSLJD37R proteins, AAZ92408 encodes murine Rank-like
CC protein RANKL, and AAZ92409-292411 encode human RANKL proteins
XX
SQ Sequence 2877 BP; 636 A; 817 C; 751 G; 673 T; 0 U; 0 Other;

Query Match 93.3%; Score 544.8; DB 3; Length 2877;
Best Local Similarity 97.4%; Pred. No. 1e-117;
Matches 571; Conservative 0; Mismatches 13; Indels 2; Gaps 2;
QY 1 GCGNCCGCGNNGNGCAAGGTCTGAGCGCCCTAGNGCCTCCCTTGGCGCTCCCTCC 60
Db 199 GCGCGCGCGCGCTGGCGAGTGTCTGAGCGCCCTAGAGCCTCCCTTGGCGCTCCCTCC 258
QY 61 TCTGCCCGCGCTAGCAGTGCACATGGGGTGTGGAGGTAGATGGGCTCCCGG-CCGGGA 119
Db 259 TCTGCCCGCGCGCAGCAGTGCACATGGGGTGTGGAGGTAGATGGGCTCCCGGCGGGA 318
QY 120 GCGCGCGGTGGATGCGCGCTGGGCGAGCAGCAGCCCGATTCACGTGCGCGCGCGCC 179
Db 319 GCGCGCGGTGGATGCGCGCTGGGCGAGCAGCAGCCCGATTCACGTGCGCGCGCGCC 378
QY 180 CC-GGCCACCTTCGAGTCCCGGTTCCAGCATGGGGACCTCTCCGAGCAGCAGCACCGC 238
Db 379 CCGGCGCGCCCTCGAGTCCCGGTTCCAGCATGGGGACCTCTCCGAGCAGCAGCACCGC 438
QY 239 CTTGCGCTCTCTGAGCGCGCATGCGCGCGAGCAGCAGCAGCATGATCGCGGCTCCCT 298
Db 439 CTTGCGCTCTCTGAGCGCGCATGCGCGCGAGCAGCAGCAGCATGATCGCGGCTCCCT 498

Qy 299 TCTCTGCTGGATTCTTACACACACACAGCTCAGCCAGAAACAGAGGCTCGAATCT 358
 Db 499 TCTCTGCTGGATTCTTACACACACACAGCTCAGCCAGAAACAGAGGCTCGAATCT 558
 Qy 359 CATTTGGACATACCGCCATGTTGACCGTGCACCGGCGAGGTCTACCTGTGACAAAGT 418
 Db 559 CATTTGGACATACCGCCATGTTGACCGTGCACCGGCGAGGTCTACCTGTGACAAAGT 618
 Qy 419 TCCAGCAGGAACCTATGCTCTGAGCATTTGTACCAACAGCCTGCGCGTCTGACGAG 478
 Db 619 TCCAGCAGGAACCTATGCTCTGAGCATTTGTACCAACAGCCTGCGCGTCTGACGAG 678
 Qy 479 TTGCCCTGTGGGACCTTTACCGAGCATGGAATGATGAGAAATGCCATGACTGTAG 538
 Db 679 TTGCCCTGTGGGACCTTTACCGAGCATGGAATGATGAGAAATGCCATGACTGTAG 738
 Qy 539 TCAGCCATGCCATGGCCATGATTGAGAAATACCTTGTGCTGCC 584
 Db 739 TCAGCCATGCCATGGCCATGATTGAGAAATACCTTGTGCTGCC 784

RESULT 11

AAL53945
 ID AAL53945 standard; DNA; 2877 BP.

XX AC AAL53945;

XX AC AAL53945;

XX 18-FEB-2003 (first entry)

XX 2877nt long primate DNA sequence.

XX Cytostatic; dermatological; antiinflammatory; immunosuppressive;
 KW antigenic; forensic analysis; abnormal physiology; autoimmune disorder;
 KW development; abnormal proliferation; cancerous; degenerative;
 KW systemic lupus erythematosus; inflammation; chromosomal mapping;
 KW drug screening; gene therapy; gene; ds.

XX Primates.

XX Key Location/Qualifiers
 FT CDS 410..2377

FT FT /tag= b
 FT /product= "655 long primate protein"

FT sig_peptide 410..532

FT mat_peptide 533..2374

FT /*tag= c

XX US2002143147-A1.

XX 03-OCT-2002.

XX 23-APR-2001; 2001US-00840795.

XX 13-JUL-1998; 98US-0092658P.

XX 23-JUL-1998; 98US-0093897P.

XX 11-SEP-1998; 98US-0099999P.

XX 12-JUL-1999; 99US-00351777.

XX (MURP/) MURPHY E E.

XX (MATT/) MATTSON J D.

XX (BATE/) BATES E E M.

XX (GORM/) GORMAN D M.

XX (LEBE/) LEBECQUE S J E.

XX Murphy EE, Mattson JD, Bates EEM, Gorman DM, Lebecque SJE;

XX WPI; 2003-102547/09.

XX P-PSDB; AAO26523.

XX New isolated or recombinant polynucleotide encoding an antigenic
 PT polypeptide, e.g. HDTBA84, HSLJD37R or RANKL polypeptide, useful for

PT regulating activation, development, differentiation and function of
 XX various cells types.

XX Claim 3; Page 33-36; 51pp; English.

XX The invention relates to an isolated or recombinant polynucleotide
 CC encoding an antigenic polypeptide comprising at least 17 contiguous amino
 CC acids from the mature polypeptide from a sequence having 300, 210, 655,
 CC 444 or 150 amino acids fully defined in the specification, or from the
 CC polypeptide from a sequence having 132, 77 or 231 amino acids given in
 CC the specification. The polynucleotide is useful in forensic analysis,
 CC e.g. to identify species or to separate different cell subsets or types.
 CC The polynucleotide, polypeptide or antibody may also be used in
 CC regulating activation, development, differentiation and function of
 CC various cell types, including haematopoietic cells, or in diagnosing or
 CC treating conditions associated with abnormal physiology or development,
 CC including abnormal proliferation, e.g. in cancerous, degenerative or
 CC autoimmune disorders (such as systemic lupus erythematosus or
 CC inflammation). They are also useful in drug screening assays and
 CC chromosomal mapping. The polynucleotide sequences of the invention can be
 CC used in gene therapy to treat disorders. This polynucleotide sequence
 CC represents a 2877nt long primate DNA relating to the antigenic proteins
 CC of the invention

XX SQ Sequence 2877 BP; 636 A; 817 C; 751 G; 673 T; 0 U; 0 Other;

Query Match 93.3%; Score 544.8; DB 8; Length 2877;

Best Local Similarity 97.4%; Pred. No. 1e-117;

Matches 571; Conservative 0; Mismatches 13; Indels 2; Gaps 2;

Qy 1 GCGNCCGCGNNGNGCAAGGTCTGAGCGCCCTTAGNGCCTCCCTTGGCGCCTCCCTCC 60
 Db 199 GCGCGCGCGCGCTGGGAGGTCTGAGCGCCCTTAGCGCCTCCCTTGGCGCCTCCCTCC 258
 Qy 61 TCTGCCCGCGCTAGAGTGCACATGGGGTGTGGAGGTAGATGGGTCCCGG-CCGGGA 119
 Db 259 TCTGCCCGCGCGAGTGCACATGGGGTGTGGAGGTAGATGGGTCCCGGCGCGGGA 318
 Qy 120 GCGCGCGGTGGATGCGCGCTGGGAGAGACAGCCCGGATTCAGCTGCCCGCGCGGCC 179
 Db 319 GCGCGGTGGATGCGCGCTGGGAGAGACAGCCCGGATTCAGCTGCCCGCGCGGCC 378
 Qy 180 CC-GGCGACCTTCGAGTCCCGGTTTCAGCATGGGGACCTCTCCGAGCAGCAGCAGCGC 238
 Db 379 CCGGCGCGCCCTCGAGTCCCGGTTTCAGCATGGGGACCTCTCCGAGCAGCAGCAGCGC 438
 Qy 239 CCTCGCTCTCTGAGCGGATTCGCGCGGAGCAGCCAGCCAGATGATCGCGGCTCCCT 298
 Db 439 CCTCGCTCTCTGAGCGGATTCGCGCGGAGCAGCCAGCCAGATGATCGCGGCTCCCT 498
 Qy 299 TCTCTGCTTGGATTCTTAGCACACACAGCTGACCGCGGCGAGGTGCTAACCTGTGACAAAGT 358
 Db 499 TCTCTGCTTGGATTCTTAGCACACACAGCTGACCGCGGCGAGGTGCTAACCTGTGACAAAGT 558
 Qy 359 CATTTGGACATACCGCCATGTTGACCGTGCACCGGCGAGGTCTACCTGTGACAAAGT 418
 Db 559 CATTTGGACATACCGCCATGTTGACCGTGCACCGGCGAGGTCTACCTGTGACAAAGT 618
 Qy 419 TCCAGCAGGAACCTATGCTCTGAGCATTTGTACCAACAGCCTGCGCGTCTGACGAG 478
 Db 619 TCCAGCAGGAACCTATGCTCTGAGCATTTGTACCAACAGCCTGCGCGTCTGACGAG 678
 Qy 479 TTGCCCTGTGGGACCTTTACCGAGCATGGAATGATGAGAAATGCCATGACTGTAG 538
 Db 679 TTGCCCTGTGGGACCTTTACCGAGCATGGAATGATGAGAAATGCCATGACTGTAG 738
 Qy 539 TCAGCCATGCCATGGCCATGATTGAGAAATACCTTGTGCTGCC 584
 Db 739 TCAGCCATGCCATGGCCATGATTGAGAAATACCTTGTGCTGCC 784

RESULT 12
 AAV99927

ID AAV99927 standard; DNA; 3474 BP.
 XX
 AC AAV99927;
 XX
 XT 10-MAY-1999 (first entry)
 XX
 DE Novel human tumor necrosis factor receptor TR9.
 XX
 KW Human; tumour necrosis factor receptor; TNFR; TR9 receptor; cancer;
 KW apoptosis; agonist; inhibition; autoimmune disorder; viral infection;
 KW inflammation; antagonist; AIDS; neurodegenerative disorder; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 247..2214
 FT /*tag= a
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 FT sig_peptide 247..366
 FT /*tag= b
 FT mat_peptide 367..2214
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 XX
 PN WO9856892-A1.
 XX
 XX 17-DEC-1998.
 XX
 XX 10-JUN-1998; 98WO-US011932.
 XX
 XX 11-JUN-1997; 97US-0052991P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Ni J, Yu G, Fan P, Gentz RL;
 XX
 DR WPI; 1999-060325/05.
 DR P-PSDB; AAW81059.
 XX
 PT New isolated tumour necrosis factor-like receptor, TR9 - used to develop
 PT products for treating e.g. cancers, autoimmune disorders, viral
 PT infections, inflammation, graft rejection, neurodegenerative disorders or
 PT ischaemic injury.
 XX
 PS Claim 2; Fig 1; 134pp; English.

This is the nucleotide sequence of the human tumour necrosis factor
 receptor (TNFR), TR9 receptor, used in the method of the invention to
 develop products to treat disorders such as cancers. The novel TNFR, TR9,
 can be used to identify agents for modifying apoptosis. Agonists can be
 used to treat diseases associated with increased cell survival, or the
 inhibition of apoptosis, including cancers (e.g. follicular lymphomas,
 carcinomas with p53 mutations, and hormone-dependent tumours, such as
 breast cancer, prostate cancer, Kaposi's sarcoma and ovarian cancer),
 autoimmune disorders (e.g. systemic lupus erythematosus and immune-
 related glomerulonephritis rheumatoid arthritis), viral infections (e.g.
 herpes viruses, pox viruses and adenoviruses), inflammation, graft vs
 host disease, acute graft rejection and chronic graft rejection.
 Antagonists can be used to treat diseases associated with increased
 apoptosis including AIDS, neurodegenerative disorders (e.g. Alzheimer's
 disease, Parkinson's disease, amyotrophic lateral sclerosis, retinitis
 pigmentosa, cerebellar degeneration), myelodysplastic syndromes (e.g.
 aplastic anemia), ischemic injury (e.g. that caused by myocardial
 infarction, stroke and reperfusion injury), toxin-induced liver disease
 (e.g. that caused by alcohol), septic shock, cachexia, anorexia,
 inflammatory diseases and stress response related diseases, such as
 inflammatory bowel disease, rheumatoid arthritis, osteoarthritis,
 psoriasis and septicemia. The products can also be used for detection and
 diagnosis

SQ Sequence 3474 BP; 832 A; 895 C; 844 G; 903 T; 0 U; 0 Other;
 Query Match 93.3%; Score 544.8; DB 2; Length 3474;
 Best Local Similarity 97.4%; Pred. No. 1e-117;

Matches 571; Conservative 0; Mismatches 13; Indels 2; Gaps 2;
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 QY 36 GCGGCGCGCGCGCTGGGCAAGGTGCTGAGCGCCCTAGAGCCCTCCCTTGGCGGCTCCCTCC 95
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 QY 61 TCTGCCCGCGCGCTAGCAGTGACATGGGGTGTGTGGAGGTAGATGGGCTCCCGG-CGGGA 119
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 QY 96 TCTGCCCGCGCGCGCAGCAGTGACATGGGGTGTGTGGAGGTAGATGGGCTCCCGGCGGGA 155
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 QY 156 GCGCGCGGTGGATGCGGCGCTGGGAGAGCAGCGCGGATTCACAGTGTCCCGCGCGCGC 215
 DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 180 CC-GGCCACCTTGGAGTCCCGGTTCCAGCCATGGGACCTCTCCGAGCAGCAGCACCGC 238
 DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 216 CCGGCGCGCGCTGCGAGTCCCGGTTCCAGCCATGGGACCTCTCCGAGCAGCAGCACCGC 275
 DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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 QY 359 CATTTGGACATACCGCATGTTGACCGTCCACCGCGCAGGTGCTAACTGTGACAAGTG 418
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 QY 419 TCCAGCAGGAACCTATGCTCTGAGCATTTGTACCAACAGCCTGCGGCTGTCAGCAG 478
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 AAA99658
 ID AAA99658 standard; cDNA; 3474 BP.
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 AC AAA99658;
 XX
 DT 02-FEB-2001 (first entry)
 XX
 DE Human tumour necrosis factor receptor TR9 cDNA.
 XX
 KW Human; tumour necrosis factor; TR9 receptor; immunosuppressive;
 KW antiinflammatory; cardiant; antiasthmatic; antidiabetic; antiallergic;
 KW antithratic; antirheumatic; anti-HIV; anticonvulsant; cytostatic;
 KW neuroprotective; gene therapy; Death Domain Containing Receptor 6;
 KW common variable immunodeficiency; X-linked agammaglobulinemia;
 KW severe combined immunodeficiency; Wiskott-Aldrich syndrome;
 KW autoimmune disease; rheumatoid arthritis; allergic encephalomyelitis;
 KW multiple sclerosis; diabetes mellitus; asthma; epilepsy; cancer;
 KW cardiovascular disease; neurological disease; protein coordinate data;
 KW ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
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 FT /*tag= a "TR9 receptor"
 FT /product= a
 FT sig_peptide 247..366
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CC indexer using the source data given in table 14 of the specification.

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XX SQ Sequence 3662 BP; 864 A; 960 C; 899 G; 939 T; 0 U; 0 Other;
      Query Match      93.3%; Score 544.8; DB 11; Length 3662;
      Best Local Similarity 97.4%; Pred. No. 1.1e-117;
      Matches 571; Conservative 0; Mismatches 13; Indels 2; Gaps 2;

QY 1 GCGGCCGCGGNGNGNCAAGGTGCTGAGCGCCCTAGNCCCTTCCCTTGGCGGCTCCCTCC 60
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QY 61 TCTGCCGCGCGCTAGCAGTGCACATGGGGTGTGGAGGTAGATGGCTCCCGG-CGGGA 119
Db 283 TCTGCCGCGCGCGAGCAGTGCACATGGGGTGTGGAGGTAGATGGCTCCCGGCCGGGA 342

QY 120 GCGCGCGGTGGATGCGCGCGCTGGGCGAGAGCAGCCCGCATTCACGCTGCGCCCGCGCGCC 179
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QY 180 CC-GGCCACCTTTCGAGTCCCGGTTTCAGCATGGGGACCTCTCCGAGCAGCAGCACCGC 238
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QY 239 CCTCGCCTCTGCGAGCGCATCGCCGCGAGCCAGCCAGCAGCATGATCGCGGCTCCCT 298
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QY 299 TCTCCTGCTTGGATTCCTTAGCACCCACAGCTCAGCCAGCAAGAGGCTTCGAATCT 358
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QY 359 CATTGGCAGATACCGGCATGTTGACCGTGCCACCGCGAGGTCTTAACCTGTGACAAAGTG 418
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QY 419 TCCAGCAGGAACCTATGCTCTCAGCATTTACCAACACAGCGCTCGGCTGTGCAGCAG 478
Db 643 TCCAGCAGGAACCTATGCTCTCAGCATTTACCAACACAGCGCTCGGCTGTGCAGCAG 702

QY 479 TTGCCCTGTGGGACCTTTACAGGCATGAGAAATGGCATAGAGAAATGCCATGACTGTAG 538
Db 703 TTGCCCTGTGGGACCTTTACAGGCATGAGAAATGGCATAGAGAAATGCCATGACTGTAG 762

QY 539 TCAGCATGCCCATGCCAATGATTGAGAAATTAACCTGTGCTGCC 584
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RESULT 15

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ID AAZ33945 standard; cDNA; 3534 BP.

XX AAZ33945;

XX DT 07-DEC-1999 (first entry)

XX DE Human PRO868 nucleotide sequence.

XX Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
KW secreted protein; transmembrane protein; ss.

XX OS Homo sapiens.

XX PN WO9946281-A2.

XX PD 16-SEP-1999.

XX PF 08-MAR-1999; 99WO-US0005028.

XX PR 10-MAR-1998; 98US-0077450P.

PR 11-MAR-1998; 98US-0077632P.

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PR 11-MAR-1998; 98US-0077641P.
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PR 30-JUL-1998; 98US-0094651P.
PR 11-SEP-1998; 98US-0100038P.
XX
PA (GETH) GENENTECH INC.
XX
XX Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
XX
XX WPI; 1999-551358/46.
DR P-PSDB; AAY41693.
XX
XX New secreted and transmembrane polypeptides and their polynucleotides,
PT useful for treating blood coagulation disorders, cancers and cellular
PT adhesion disorders.
XX
XX Claim 2; Fig 25; 530pp; English.
XX
XX

CC The present invention describes secreted and transmembrane polypeptides
CC and their polynucleotides. The nucleotide sequences are useful as sources
CC of probes, primers, for chromosome mapping, and for generation of
CC antisense sequences. They can also be used to create transgenic animals.
CC The proteins can be used to treat a variety of diseases and disorders,
CC depending on their function. Diseases that may be treated include blood
CC coagulation disorders, cancers and cellular adhesion disorders. They may
CC also be used to raise antibodies. AA233891 to AA234338, and AA41685 to
CC AA41774 represent polynucleotide and polypeptide sequence given in the
CC exemplification of the present invention
XX
XX

SQ Sequence 3534 BP; 829 A; 927 C; 858 G; 920 T; 0 U; 0 Other;

Query Match 93.0%; Score 543.2; DB 2; Length 3534;
Best Local Similarity 97.3%; Pred. No. 2.5e-117;
Matches 570; Conservative 0; Mismatches 14; Indels 2; Gaps 2;
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DB 294 CCGGCGCGCCCTCGGAGTCCCGGTTCAGCCATGGGGACCTCTCCGAGCAGCAGCAGCCG 353
QY 239 CTTGCGCTCTGAGCGCGCATGCGCGCGCGCGAGCCACAGCCAGCATGATCGGGGCTCCCT 298
DB 354 CTTGCGCTCTGAGCGCGCATGCGCGCGCGCGAGCCACAGCCAGCATGATGCGGGCTCCCT 413
QY 299 TCTCTGCTTGGATTCTTACGACCCAGCAGCTCAGCCAGCAGCAGAGGCTCGATCT 358
DB 414 TCTCTGCTTGGATTCTTACGACCCAGCAGCTCAGCCAGCAGCAGAGGCTCGATCT 473
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GenCore version 5.1.6
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SUMMARIES

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C 43	40.4	6.9	700	3	US-09-236-097-7	Sequence 7, Appli
C 44	40.4	6.9	4403765	3	US-09-103-840A-2	Sequence 2, Appli
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ALIGNMENTS

RESULT 1
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; Sequence 3, Application US/08959382
; Patent No. 6013476
; GENERAL INFORMATION:
; APPLICANT: DEEN, KEITH
; APPLICANT: HURLE, MARK
; APPLICANT: YOUNG, PETER
; APPLICANT: TAN, K.B.
; TITLE OF INVENTION: Tumor Necrosis Related Receptor,
; TITLE OF INVENTION: TR7
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/959,382
; FILING DATE: 28-OCT-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/041,796
; FILING DATE: 02-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-50017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 584 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-959-382-3

Query Match 99.0%; Score 578; DB 3; Length 584;
Best Local Similarity 100.0%; Pred. No. 1.8e-135;

Matches 584; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGNCCGCGGNGNGCAAGGTGCTGAGCGCCCTAGNGCCTCCCTTGGCGGCTCCCTCC 60
DB 1 GCGNCCGCGGNGNGCAAGGTGCTGAGCGCCCTAGNGCCTCCCTTGGCGGCTCCCTCC 60

QY 61 TCTGCCCGGCGGTAGCAGTGACATGGGGTGTGGAGGTAGATGGGCTCCCGCGCGGAG 120
DB 61 TCTGCCCGGCGGTAGCAGTGACATGGGGTGTGGAGGTAGATGGGCTCCCGCGCGGAG 120

QY 121 GCGGCGGTGGATGCGGCGTGGGCGAGAACAGCGCGCGATTCAGCTGCGCGCGGCC 180
DB 121 GCGGCGGTGGATGCGGCGTGGGCGAGAACAGCGCGCGATTCAGCTGCGCGCGGCC 180

QY 181 GCGGCGGTGGATGCGGCGTGGGCGAGAACAGCGCGCGATTCAGCTGCGCGCGGCC 240
DB 181 GCGGCGGTGGATGCGGCGTGGGCGAGAACAGCGCGCGATTCAGCTGCGCGCGGCC 240

QY 241 TCGCCTCTCTGAGCGCGATCGCGCGGAGCCACAGCGCGATGATCGCGGCTCCCTTC 300
DB 241 TCGCCTCTCTGAGCGCGATCGCGCGGAGCCACAGCGCGATGATCGCGGCTCCCTTC 300

QY 301 TCTGCTTGGATTCCTTAGCACACACAGCTCAGCGAGAACAGAGGCTCGAATCTCA 360
DB 301 TCTGCTTGGATTCCTTAGCACACACAGCTCAGCGAGAACAGAGGCTCGAATCTCA 360

QY 361 TTGGCACATACCGCCATGTTGACCGTGGCCACCGCGGAGGTGCTAACTGTGACAGTGC 420
DB 361 TTGGCACATACCGCCATGTTGACCGTGGCCACCGCGGAGGTGCTAACTGTGACAGTGC 420

QY 421 CAGCAGGAACCTATGCTCTGAGCATTTACCAACACAGCGCTCGCGCTCTGAGCAGTT 480
DB 421 CAGCAGGAACCTATGCTCTGAGCATTTACCAACACAGCGCTCGCGCTCTGAGCAGTT 480

QY 481 GCGCTGTGGGACCTTTACAGGCATGAGAAATGAGAAATGCCATGACTGTAGTC 540
DB 481 GCGCTGTGGGACCTTTACAGGCATGAGAAATGAGAAATGCCATGACTGTAGTC 540

QY 541 AGCCATGCCCATGGCCAAATGATTGAGAAATACCTTGTGCTGCC 584
DB 541 AGCCATGCCCATGGCCAAATGATTGAGAAATACCTTGTGCTGCC 584

RESULT 2

US-314-844F-3
; Sequence 3, Application US/09314844F
; Patent No. 6660839
; GENERAL INFORMATION:
; APPLICANT: DEEN, KEITH CHARLES
; APPLICANT: HURLE, MARK R.
; APPLICANT: YOUNG, PETER
; APPLICANT: TAN, K. B.
; TITLE OF INVENTION: DNA ENCODING TUMOR NECROSIS RELATED
; FILE OF INVENTION: RECEPTOR TR7
; CURRENT APPLICATION NUMBER: US/09/314,844F
; FILE REFERENCE: GH-50017-1
; CURRENT FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 60/041,796
; PRIOR FILING DATE: 1997-04-02
; PRIOR APPLICATION NUMBER: US 08/959,382
; PRIOR FILING DATE: 1997-10-28
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 584
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (4) (10) (11) (13) (15) (38)
; OTHER INFORMATION: OTHER INFORMATION: n= a, g, c or t

Query Match 99.0%; Score 578; DB 4; Length 584;
Best Local Similarity 100.0%; Pred. No. 1.8e-135; Mismatches 0; Indels 0; Gaps 0;
Matches 584; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGNCCGCGGNGNGCAAGGTGCTGAGCGCCCTAGNGCCTCCCTTGGCGGCTCCCTCC 60
DB 1 GCGNCCGCGGNGNGCAAGGTGCTGAGCGCCCTAGNGCCTCCCTTGGCGGCTCCCTCC 60

QY 61 TCTGCCCGGCGGTAGCAGTGACATGGGGTGTGGAGGTAGATGGGCTCCCGCGCGGAG 120
DB 61 TCTGCCCGGCGGTAGCAGTGACATGGGGTGTGGAGGTAGATGGGCTCCCGCGCGGAG 120

QY 121 GCGGCGGTGGATGCGGCGTGGGCGAGAACAGCGCGCGATTCAGCTGCGCGCGGCC 180
DB 121 GCGGCGGTGGATGCGGCGTGGGCGAGAACAGCGCGCGATTCAGCTGCGCGCGGCC 180

QY 181 GCGGCGGTGGATGCGGCGTGGGCGAGAACAGCGCGCGATTCAGCTGCGCGCGGCC 240
DB 181 GCGGCGGTGGATGCGGCGTGGGCGAGAACAGCGCGCGATTCAGCTGCGCGCGGCC 240

QY 241 TCGCCTCTCTGAGCGCGATCGCGCGGAGCCACAGCGCGATGATCGCGGCTCCCTTC 300
DB 241 TCGCCTCTCTGAGCGCGATCGCGCGGAGCCACAGCGCGATGATCGCGGCTCCCTTC 300

QY 301 TCTGCTTGGATTCCTTAGCACACACAGCTCAGCGAGAACAGAGGCTCGAATCTCA 360
DB 301 TCTGCTTGGATTCCTTAGCACACACAGCTCAGCGAGAACAGAGGCTCGAATCTCA 360

QY 361 TTGGCACATACCGCCATGTTGACCGTGGCCACCGCGGAGGTGCTAACTGTGACAGTGC 420
DB 361 TTGGCACATACCGCCATGTTGACCGTGGCCACCGCGGAGGTGCTAACTGTGACAGTGC 420

QY 421 CAGCAGGAACCTATGCTCTGAGCATTTACCAACACAGCGCTCGCGCTCTGAGCAGTT 480
DB 421 CAGCAGGAACCTATGCTCTGAGCATTTACCAACACAGCGCTCGCGCTCTGAGCAGTT 480

QY 481 GCGCTGTGGGACCTTTACAGGCATGAGAAATGAGAAATGCCATGACTGTAGTC 540
DB 481 GCGCTGTGGGACCTTTACAGGCATGAGAAATGAGAAATGCCATGACTGTAGTC 540

QY 541 AGCCATGCCCATGGCCAAATGATTGAGAAATACCTTGTGCTGCC 584
DB 541 AGCCATGCCCATGGCCAAATGATTGAGAAATACCTTGTGCTGCC 584

RESULT 3

US-09-314-844F-5
; Sequence 5, Application US/09314844F
; Patent No. 6660839
; GENERAL INFORMATION:
; APPLICANT: DEEN, KEITH CHARLES
; APPLICANT: HURLE, MARK R.
; APPLICANT: YOUNG, PETER
; APPLICANT: TAN, K. B.
; TITLE OF INVENTION: DNA ENCODING TUMOR NECROSIS RELATED
; FILE OF INVENTION: RECEPTOR TR7
; CURRENT APPLICATION NUMBER: US/09/314,844F
; CURRENT FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 60/041,796
; PRIOR FILING DATE: 1997-04-02
; PRIOR APPLICATION NUMBER: US 08/959,382
; PRIOR FILING DATE: 1997-10-28
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 588
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (4) (10) (11) (13) (15) (38)
; OTHER INFORMATION: OTHER INFORMATION: n= a, g, c or t

US-09-314-844F-5

Query Match 94.2%; Score 550.2; DB 4; Length 588;
Best Local Similarity 98.5%; Pred. No. 1.6e-128;
Matches 572; Conservative 0; Mismatches 8; Indels 1; Gaps 1;
QY 1 GCNCCGCGNNGNGCAAGTGTCTGAGCGCCCTTAGNGCCTCTCCCTTGGCGCTCCCTCC 60
DB 1 GCNCCGCGNNGNGCAAGTGTCTGAGCGCCCTTAGNGCCTCTCCCTTGGCGCTCCCTCC 60
QY 61 TCTGCGCGCGTAGCAGTGCACATGGGGTGTGGAGGTAGATGGCTCCCGCGCGGAG 120
DB 61 TCTGCGCGCGTAGCAGTGCACATGGGGTGTGGAGGTAGATGGCTCCCGCGCGGAG 120
QY 121 GCAGCGGTGATGCGCGCTGGCGCAGAGCAGCGCGCGGATTCAGCTGCGCGCGCGCC 180
DB 121 GCAGCGGTGATGCGCGCTGGCGCAGAGCAGCGCGCGGATTCAGCTGCGCGCGCGCC 180
QY 181 CGGCCACCTTGGAGTCCCGGTTCAGCCATGCGGACCTTCCGAGCAGCAGCGCGCC 240
DB 181 CGGCCACCTTGGAGTCCCGGTTCAGCCATGCGGACCTTCCGAGCAGCAGCGCGCC 240
QY 241 TC-GCTCTCTGAGCGCATGCGCGCGCGGACGAGCGCGCGGATTCAGCTGCGCGCGCT 299
DB 241 TC-GCTCTCTGAGCGCATGCGCGCGCGGACGAGCGCGCGGATTCAGCTGCGCGCGCT 299
QY 300 CTCTGCTGCTGATTCCTTAGCACACACAGCTCAGCGAGCAGAGAGGCTCGAATCTC 359
DB 301 CTCTGCTGCTGATTCCTTAGCACACACAGCTCAGCGAGCAGAGAGGCTCGAATCTC 360
QY 360 ATTGGCACATPACCGCATGTTGACCGTGCACCGCGCGGAGTGTAACTGTGCAAGTGT 419
DB 361 ATTGGCACATPACCGCATGTTGACCGTGCACCGCGCGGAGTGTAACTGTGCAAGTGT 420
QY 420 CAGCAGGACCTATGCTCTGAGCATTTGACCAACAGAGCTGCGGCTGCGAGCAGT 479
DB 421 CAGCAGGACCTATGCTCTGAGCATTTGACCAACAGAGCTGCGGCTGCGAGCAG 480
QY 480 TGCCTGTGGGACCTTTACAGGCATGAGAAATGAGAAATGAGAAATGAGAAATGAGT 539
DB 481 TGCCTGTGGGACCTTTACAGGCATGAGAAATGAGAAATGAGAAATGAGAAATGAGT 540
QY 540 CAGCCATGCCCATTGGCCAAATGATTGAGAAATTAACCTTTGTGC 580
DB 541 CAGCCATGCCCATTGGCCAAATGATTGAGAAATTAACCTTTGTGC 581

RESULT 4

US-09-042-785A-22
; Sequence 22, Application US/09042785A
; Patent No. 6194151
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J
; TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
; TITLE OF INVENTION: AND USES THEREFOR
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,785A
; FILING DATE: 17-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/938,896

FILING DATE: 26-SEP-1997
ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MEI-001CP
TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2638 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 510..2327
US-09-042-785A-22

Query Match 93.3%; Score 544.8; DB 3; Length 2638;
Best Local Similarity 97.4%; Pred. No. 5.4e-127;
Matches 571; Conservative 0; Mismatches 13; Indels 2; Gaps 2;
QY 1 GCNCCGCGNNGNGCAAGTGTCTGAGCGCCCTTAGNGCCTCTCCCTTGGCGCTCCCTCC 60
DB 299 GCGCGCGCGCGCTGGCGAGGTGCTGAGCGCCCTTAGAGCTCCCTTGGCGCTCCCTCC 358
QY 61 TCTGCGCGCGCTAGCAGTGCACATGGGGTGTGGAGGTAGATGGCTCCCGG-CCGGGA 119
DB 359 TCTGCGCGCGCGCTAGCAGTGCACATGGGGTGTGGAGGTAGATGGCTCCCGG-CCGGGA 418
QY 120 GCGCGCGGTGGATGCGCGCTGGCGCAGAGCAGCGCCGATTCAGCTGCGCGCGCGGCC 179
DB 419 GCGCGCGGTGGATGCGCGCTGGCGCAGAGCAGCGCCGATTCAGCTGCGCGCGCGGCC 478
QY 180 CC-GGCGACCTTTCGAGTCCCGGTTCAGCCATGCGGACCTCTCCGAGCAGCAGCAGCGC 238
DB 479 CCGCGCGCGCTTCGAGTCCCGGTTCAGCCATGCGGACCTCTCCGAGCAGCAGCAGCGC 538
QY 239 CCGCGCGCTTCGAGCAGCGCATGCGCGCGCGGAGCAGCAGCAGCAGCAGCAGCAGC 298
DB 539 CCGCGCGCTTCGAGCAGCGCATGCGCGCGCGGAGCAGCAGCAGCAGCAGCAGCAGC 598
QY 299 TCTCTGCTTGGATTCCTTAGCAGCAGCAGCTCAGCGCAGAGCAGAGAGCCTCGAATCT 358
DB 599 TCTCTGCTTGGATTCCTTAGCAGCAGCAGCTCAGCGCAGAGCAGAGAGCCTCGAATCT 658
QY 359 CATTGGCACATACCGCCATGTTGACCGTCCACCGCGCAGGTGCTAACTGTGACAAAGTG 418
DB 659 CATTGGCACATACCGCCATGTTGACCGTCCACCGCGCAGGTGCTAACTGTGACAAAGTG 718
QY 419 TCAGCAGAGAACCTATGCTCTGAGCATTTGATACCAACAGCAGCAGCAGCAGCAGCAG 478
DB 719 TCAGCAGAGAACCTATGCTCTGAGCATTTGATACCAACAGCAGCAGCAGCAGCAGCAG 778
QY 479 TTGCGCTGTGGGACCTTTACAGGCATGAGAAATGAGAAATGAGAAATGAGAAATGAGT 538
DB 779 TTGCGCTGTGGGACCTTTACAGGCATGAGAAATGAGAAATGAGAAATGAGAAATGAGT 838
QY 539 TCAGCCATGCCCATGGCCAAATGATTGAGAAATTAACCTTTGTGTGCC 584
DB 839 TCAGCCATGCCCATGGCCAAATGATTGAGAAATTAACCTTTGTGTGCC 884

RESULT 5

US-09-527-236A-1
; Sequence 1, Application US/09527236A
; Patent No. 6358508
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Pan, Ping

APPLICANT: Gentz, Reiner L.
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
FILE REFERENCE: PF375P1
CURRENT APPLICATION NUMBER: US/09/527,236A
CURRENT FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/052,991
PRIOR FILING DATE: 1997-06-11
PRIOR APPLICATION NUMBER: 09/095,094
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/126,019
PRIOR FILING DATE: 1999-03-24
PRIOR APPLICATION NUMBER: 60/134,220
PRIOR FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 3474
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (247)..(2211)
NAME/KEY: sig_peptide
LOCATION: (247)..(366)
NAME/KEY: mat_peptide
LOCATION: (367)..(2211)
US-09-527-236A-1

Query Match 93.3%; Score 544.8; DB 3; Length 3474;
Best Local Similarity 97.4%; Pred. No. 5.7e-127;
Matches 571; Conservative 0; Mismatches 13; Indels 2; Gaps 2;
QY 1 GCGNCCGCGNNGNGCAAGTGCTGAGCGCCCTAGNGCCTCCCTGCGCGCTCCCTCC 60
Db 36 GCGCGCGCGCGCTGGCAGGTGCTGAGCGCCCTAGAGCCTCCCTTGGCGCTCCCTCC 95
QY 61 TCTGCCCGCGCGTAGCAGTGCACATGGGGTGTGGAGGTAGATGGGTCCCGG-CGCGGA 119
Db 96 TCTGCCCGCGCGCAGCAGTGCACATGGGGTGTGGAGGTAGATGGGTCCCGGCGCGCC 155
QY 120 GCGCGCGGTGGATGCGCGCTGGGAGAGCAGCGCGCGATTCAGTGCGCGCGCGCC 179
Db 156 GCGCGCGGTGGATGCGCGCTGGGAGAGCAGCGCGCGATTCAGTGCGCGCGCGCC 215
QY 180 CC-GGCGACCTTCGAGTCCCGGTTCCAGCATGGGGACCTCTCCGAGCAGCAGCCGC 238
Db 216 CCGGGCGCGCTCGAGTCCCGGTTCCAGCATGGGGACCTCTCCGAGCAGCAGCCGC 275
QY 239 CTTGCGCTCTGTCAGCGCGCATGCGCGCGCGAGCCAGCCAGCATGATCGCGGCTCCCT 298
Db 276 CTTGCGCTCTGTCAGCGCGCATGCGCGCGCGAGCCAGCCAGCATGATCGCGGCTCCCT 335
QY 299 TCTCTCTTGGATTCTTAGCACCACACAGCTCAGCCAGAAACAGAGCCTCGAATCT 358
Db 336 TCTCTCTTGGATTCTTAGCACCACACAGCTCAGCCAGAAACAGAGCCTCGAATCT 395
QY 359 CATTTGCACATACCGCATCTTCCAGCTGCCCGCGCGAGTGTACCTGTGACAGTG 418
Db 396 CATTTGCACATACCGCATCTTCCAGCTGCCCGCGCGAGTGTACCTGTGACAGTG 455
QY 419 TCAGCAGGAACCTATGTCTCTGAGCATTTGTACAAACAGCCTCGGCTGTGACAGCAG 478
Db 456 TCAGCAGGAACCTATGTCTCTGAGCATTTGTACAAACAGCCTCGGCTGTGACAGCAG 515
QY 479 TTGCGCTGTGGGACCTTTACAGGATGAGATGAGATGAGAAATGCCATGACTGTAG 538
Db 516 TTGCGCTGTGGGACCTTTACAGGATGAGATGAGATGAGAAATGCCATGACTGTAG 575
QY 539 TCAGCAGGATGCCATGAGATGAGAAATACCTTTGTGTGCC 584
Db 576 TCAGCAGGATGCCATGAGATGAGAAATACCTTTGTGTGCC 621

RESULT 6
US-09-756-854-1
Sequence 1, Application US/09756854
Patent No. 6667390
GENERAL INFORMATION:
APPLICANT: Ni, Jian
Yu, Guo-Liang
Fan, Ping
Gentz, Reiner
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSER: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MD
COUNTRY: US
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/756,854
FILING DATE: 10-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/095,094
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Hoover, Kenley K.
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PF375
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3474 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 247..2211
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 367..2211
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 247..364
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-756-854-1

Query Match 93.3%; Score 544.8; DB 4; Length 3474;
Best Local Similarity 97.4%; Pred. No. 5.7e-127;
Matches 571; Conservative 0; Mismatches 13; Indels 2; Gaps 2;
QY 1 GCGNCCGCGNNGNGCAAGTGCTGAGCGCCCTAGNGCCTCCCTTGGCGCTCCCTCC 60
Db 36 GCGCGCGCGCGCTGGCAGGTGCTGAGCGCCCTAGAGCCTCCCTTGGCGCTCCCTCC 95
QY 61 TCTGCCCGCGCGTAGCAGTGCACATGGGGTGTGGAGGTAGATGGGTCCCGG-CGCGGA 119
Db 96 TCTGCCCGCGCGCAGCAGTGCACATGGGGTGTGGAGGTAGATGGGTCCCGGCGCGGA 155
QY 120 GCGCGCGGTGGATGCGCGCTGGGAGAGCAGCGCGATTCAGCTGCGCGCGCGCC 179
Db 156 GCGCGCGGTGGATGCGCGCTGGGAGAGCAGCGCGATTCAGCTGCGCGCGCGCC 215
QY 180 CC-GGCGACCTTTCGAGTCCCGGTTCCAGCATGGGGACCTCTCCGAGCAGCAGCCGC 238

Db 216 CCGGGCCCTCGAGTCCCGGTTCCAGCCATGGGACCTCTCCGAGCAGCAGCCGC 275
Qy 239 CCTCGCTCTGAGCGCAGCTCGCCCGCCGAGCCACAGCCAGATGATCGGGCTCCCT 298
Db 276 CCTCGCTCTGAGCGCAGCTCGCCCGCCGAGCCACAGCCAGATGATCGGGCTCCCT 335
Qy 299 TCTCTCTGTTGATTCCTTAGCACCACACAGCTCAGCCAGAAACAGAAAGCCTCGAATCT 358
Db 336 TCTCTCTGTTGATTCCTTAGCACCACACAGCTCAGCCAGAAACAGAAAGCCTCGAATCT 395
Qy 359 CATTTGGACATACCGCCATGTTGACCGTGGCCAGCCGAGTGCTAACCTGTGACAAAGTG 418
Db 396 CATTTGGACATACCGCCATGTTGACCGTGGCCAGCCGAGTGCTAACCTGTGACAAAGTG 455
Qy 419 TCCAGCAGGAACCTATGCTCTGAGCAATGTGACCAACAGCCGCTGTCGACGAG 478
Db 456 TCCAGCAGGAACCTATGCTCTGAGCAATGTGACCAACAGCCGCTGTCGACGAG 515
Qy 479 TTGCTCTGTGGGACCTTTTACCAGGCGATGAGAAATGAGAAATGCCATGACTGTAG 538
Db 516 TTGCTCTGTGGGACCTTTTACCAGGCGATGAGAAATGAGAAATGCCATGACTGTAG 575
Qy 539 TCAGCCATGCCATGGCCATGATTTAGAAATTTACCTTTGTGCTGCC 584
Db 576 TCAGCCATGCCATGGCCATGATTTAGAAATTTACCTTTGTGCTGCC 621

RESULT 7

US-09-042-785A-3
; Sequence 3, Application US/09042785A
; Patent No. 6194151
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J
; TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
; TITLE OF INVENTION: AND USES THEREFOR
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,785A
; FILING DATE: 17-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/938,896
; FILING DATE: 26-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MEI-001CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2612 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 190..951
US-09-042-785A-3

Query Match 90.7%; Score 529.4; DB 3; Length 2612;
Best Local Similarity 98.4%; Pred. No. 3.8e-123;
Matches 555; Conservative 0; Mismatches 7; Indels 2; Gaps 2;
Qy 23 GCTGAGGCGCCCTAGNGCCTCCCTTGGCGGCTCCCTCTCTGCGCGCCCTAGCAGTGCA 82
Db 1 GCTCAGCGCCCTAGACCCCTCCCTTGGCGGCTCCCTCTCTGCGCGCCCTAGCAGTGCA 60
Qy 83 CATGGGGGTGTTGAGGTAGATGGCTCCCGG-CGGGAGCGCGGTGGATGGCGCGCTG 141
Db 61 CATGGGGGTGTTGAGGTAGATGGCTCCCGGCGGAGCGCGGTGGATGGCGCGCTG 120
Qy 142 GGCAGAAAGCAGCGCCGATTTCCAGAGTCCCGCGCGCGCCC-GGCCACCTTTGCCAGTCCCC 200
Db 121 GGCAGAAAGCAGCGCCGATTTCCAGAGTCCCGCGCGCGCCCCTGCGAGTCCCC 180
Qy 201 GGTTCAGCCATGCGGACCTCTCCGAGCAGCAGCAGCCCTCGCTCTCGAGCGGATC 260
Db 181 GGTTCAGCCATGCGGACCTCTCCGAGCAGCAGCAGCCCTCGCTCTCGAGCGGATC 240
Qy 261 GCCCGCGGACCCACAGCCAGATGATCGGGCTCCCTTCTCTGCTTGAATTCCTTAGC 320
Db 241 GCCCGCGGACCCACAGCCAGATGATCGGGCTCCCTTCTCTGCTTGAATTCCTTAGC 300
Qy 321 ACCACACACAGCTCAGCCAGAAACAGAGGCTCGAATCTCATTTGGCACAATACCGCATGTT 380
Db 301 ACCACACAGCTCAGCCAGAAACAGAGGCTCGAATCTCATTTGGCACAATACCGCATGTT 360
Qy 381 GACCGTGCCACCGCCAGGTGCTAACTGTGACAAAGTGTCCAGCAGAACTATGCTCT 440
Db 361 GACCGTGCCACCGCCAGGTGCTAACTGTGACAAAGTGTCCAGCAGAACTATGCTCT 420
Qy 441 GAGCATTTACCAACACAGCCCTCGCGCTCTGAGCAGATTTGCCCTGTGGGACCTTTACC 500
Db 421 GAGCATTTACCAACACAGCCCTCGCGCTCTGAGCAGATTTGCCCTGTGGGACCTTTACC 480
Qy 501 AGGCATGAGAAATGGCATAGAAATGCCATGCTAGTCAGCCATGCCCAATGCCCAATG 560
Db 481 AGGCATGAGAAATGGCATAGAAATGCCATGCTAGTCAGCCATGCCCAATGCCCAATG 540
Qy 561 ATTGAGAAATTTACCTTTGTGCTGCC 584
Db 541 ATTGAGAAATTTACCTTTGTGCTGCC 564

RESULT 8

US-08-959-382-1
; Sequence 1, Application US/08959382
; Patent No. 6013476
; GENERAL INFORMATION:
; APPLICANT: DEEN, KEITH
; APPLICANT: HURLE, MARK
; APPLICANT: YOUNG, PETER
; APPLICANT: TAN, K. B.
; TITLE OF INVENTION: Tumor Necrosis Related Receptor,
; TITLE OF INVENTION: TR7
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P. O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/959,382
; FILING DATE: 28-OCT-1997

TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 759 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..759
US-09-042-785A-6

Query Match 64.2%; Score 375; DB 3; Length 759;
Best Local Similarity 100.0%; Pred. No. 1.1e-84;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 210 ATGGGACCTCTCCGAGCAGCAGCAGCGCCCTCGCTTCTCTGCTTGGATTCCCTTAGCACCACCA 269
Db 1 ATGGGACCTCTCCGAGCAGCAGCAGCGCCCTCGCTTCTCTGCTTGGATTCCCTTAGCACCACCA 60
QY 270 GCCACAGCCACGATGATCGGGGCTCCCTTCTCTGCTTGGATTCCCTTAGCACCACCA 329
Db 61 GCCACAGCCACGATGATCGGGGCTCCCTTCTCTGCTTGGATTCCCTTAGCACCACCA 120
QY 330 GCTCAGCCAGCAGAGGCTCGAATCTCATTTGGCACAATACCGCCATGTTGACCGTGCC 389
Db 121 GCTCAGCCAGCAGAGGCTCGAATCTCATTTGGCACAATACCGCCATGTTGACCGTGCC 180
QY 390 ACCGGCAGGTGTAACCTGTGACAAGTGTCCAGCAGGAACCTATGTTCTGAGCATTTGT 449
Db 181 ACCGGCAGGTGTAACCTGTGACAAGTGTCCAGCAGGAACCTATGTTCTGAGCATTTGT 240
QY 450 ACCAACACAGCTGCGCGCTCGAGCAGTTGCCCTGTGGGGACCTTTACCGGCATGAG 509
Db 241 ACCAACACAGCTGCGCGCTCGAGCAGTTGCCCTGTGGGGACCTTTACCGGCATGAG 300
QY 510 AATGGCATAGAGAAATGCCATGACTGTAGTCAGCCATGCCCATGGCCAAATGATTGAGAAA 569
Db 301 AATGGCATAGAGAAATGCCATGACTGTAGTCAGCCATGCCCATGGCCAAATGATTGAGAAA 360
QY 570 TTACCTTGTGCTGCC 584
Db 361 TTACCTTGTGCTGCC 375
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RESULT 11

US-09-042-785A-24
; Sequence 24, Application US/09042785A
; Patent No. 6194151
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J
; TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,785A
; FILING DATE: 17-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/938,896
; FILING DATE: 26-SEP-1997

ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MEI-001CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1815 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1815
US-09-042-785A-24

Query Match 64.2%; Score 375; DB 3; Length 1815;
Best Local Similarity 100.0%; Pred. No. 1.3e-84;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 210 ATGGGACCTCTCCGAGCAGCAGCAGCGCCCTCGCTTCTCTGCTTGGATTCCCTTAGCACCACCA 269
Db 1 ATGGGACCTCTCCGAGCAGCAGCAGCGCCCTCGCTTCTCTGCTTGGATTCCCTTAGCACCACCA 60
QY 270 GCCACAGCCACGATGATCGGGGCTCCCTTCTCTGCTTGGATTCCCTTAGCACCACCA 329
Db 61 GCCACAGCCACGATGATCGGGGCTCCCTTCTCTGCTTGGATTCCCTTAGCACCACCA 120
QY 330 GCTCAGCCAGCAGAGGCTCGAATCTCATTTGGCACAATACCGCCATGTTGACCGTGCC 389
Db 121 GCTCAGCCAGCAGAGGCTCGAATCTCATTTGGCACAATACCGCCATGTTGACCGTGCC 180
QY 390 ACCGGCAGGTGTAACCTGTGACAAGTGTCCAGCAGGAACCTATGTTCTGAGCATTTGT 449
Db 181 ACCGGCAGGTGTAACCTGTGACAAGTGTCCAGCAGGAACCTATGTTCTGAGCATTTGT 240
QY 450 ACCAACACAGCTGCGCGCTCGAGCAGTTGCCCTGTGGGGACCTTTACCGGCATGAG 509
Db 241 ACCAACACAGCTGCGCGCTCGAGCAGTTGCCCTGTGGGGACCTTTACCGGCATGAG 300
QY 510 AATGGCATAGAGAAATGCCATGACTGTAGTCAGCCATGCCCATGGCCAAATGATTGAGAAA 569
Db 301 AATGGCATAGAGAAATGCCATGACTGTAGTCAGCCATGCCCATGGCCAAATGATTGAGAAA 360
QY 570 TTACCTTGTGCTGCC 584
Db 361 TTACCTTGTGCTGCC 375
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RESULT 12

US-09-527-236A-8/c
; Sequence 8, Application US/09527236A
; Patent No. 6358508
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Fan, Ping
; APPLICANT: Gentz, Reiner L.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
; FILE REFERENCE: PF375P1
; CURRENT APPLICATION NUMBER: US/09/527,236A
; CURRENT FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/052,991
; PRIOR FILING DATE: 1997-06-11
; PRIOR APPLICATION NUMBER: 09/095,094
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/126,019
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: 60/134,220
; PRIOR FILING DATE: 1999-05-14

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; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 345
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-527-236A-8

Query Match      45.1%; Score 263.6; DB 3; Length 345;
Best Local Similarity 93.3%; Pred. No. 6e-57;
Matches 319; Conservative 0; Mismatches 19; Indels 4; Gaps 4;

QY 239 CTTGCGCTCTGAGCGGATCGCCGCGAGCCAGCCAGCATGCGCGGCTCCCT 298
Db 345 CTTGCGCTCTGAGCGGATCGCCGCGAGCCAGCCAGCATGCGCGGCTCCCT 288
QY 299 TCTCTGCTTGGATTCTTAGCACCACAGCTCAGCCAGAACAGAGGCTCGAATCT 358
Db 287 TCTCC-GCTTGGATTCTTAGCACCACAGCTCAGCCAGAACAGAGGCTCGAATCT 229
QY 359 CATTGGACATACCGGATGTTGACCGTGCACCGCCAGGTCTAACTGTGACAAGTG 418
Db 228 CATTGGACATACCGGATGTTGACCGTGCACCGCCAGGTCTAACTGTGACAAGTG 229
QY 419 TCAGCAGGAACCTATGCTCTGAGCATGTACCAACAGAGCTCGCGGTCTGACAGAG 478
Db 168 TCAGCAGGAACCTATGCTCTGAGCA-TGTACCAACAGAGCTCGCGGTCTGACAGAG 110
QY 479 TTGCGCTGTGGGACCTTTACAGGATGAGAAATGCGCAATGCGCATGCTGTAG 538
Db 109 TTGCGCTGTGGGACCTTTACAGGATGAGAAATGCGCAATGCGCATGCTGTAG 50
QY 539 TCAGCCATGCCATGCCAATGATTGAGAAATTTACCTTTGTC 580
Db 49 TCAGCCATGCCATGCCAATGATTGAGAAATTTACCTTTGTC 8

RESULT 13
US-09-756-854-8/c
; Sequence 8, Application US/09756854
; Patent No. 6667390
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; Pan, Ping
; Gentz, Reiner
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09756,854
; FILING DATE: 10-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/095,094
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoover, Kenley K.
; REGISTRATION NUMBER: 40,302
; REFERENCE/DOCKET NUMBER: PF375
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504

; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 345 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-756-854-8

Query Match      45.1%; Score 263.6; DB 4; Length 345;
Best Local Similarity 93.3%; Pred. No. 6e-57;
Matches 319; Conservative 0; Mismatches 19; Indels 4; Gaps 4;

QY 239 CTTGCGCTCTGAGCGGATCGCCGCGAGCCAGCCAGCATGCGCGGCTCCCT 298
Db 345 CTTGCGCTCTGAGCGGATCGCCGCGAGCCAGCCAGCATGCGCGGCTCCCT 288
QY 299 TCTCTGCTTGGATTCTTAGCACCACAGCTCAGCCAGAACAGAGGCTCGAATCT 358
Db 287 TCTCC-GCTTGGATTCTTAGCACCACAGCTCAGCCAGAACAGAGGCTCGAATCT 229
QY 359 CATTGGACATACCGGATGTTGACCGTGCACCGCCAGGTCTAACTGTGACAAGTG 418
Db 228 CATTGGACATACCGGATGTTGACCGTGCACCGCCAGGTCTAACTGTGACAAGTG 229
QY 419 TCAGCAGGAACCTATGCTCTGAGCATGTACCAACAGAGCTCGCGGTCTGACAGAG 478
Db 168 TCAGCAGGAACCTATGCTCTGAGCA-TGTACCAACAGAGCTCGCGGTCTGACAGAG 110
QY 479 TTGCGCTGTGGGACCTTTACAGGATGAGAAATGCGCAATGCGCATGCTGTAG 538
Db 109 TTGCGCTGTGGGACCTTTACAGGATGAGAAATGCGCAATGCGCATGCTGTAG 50
QY 539 TCAGCCATGCCATGCCAATGATTGAGAAATTTACCTTTGTC 580
Db 49 TCAGCCATGCCATGCCAATGATTGAGAAATTTACCTTTGTC 8

RESULT 14
US-09-042-785A-1
; Sequence 1, Application US/09042785A
; Patent No. 6194151
; GENERAL INFORMATION:
; APPLICANT: Bugfield, Samantha J
; TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,785A
; FILING DATE: 17-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/938,896
; FILING DATE: 26-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MEI-001CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
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TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3331 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 344..2065
; US-09-042-785A-1

Query Match 39.5%; Score 230.8; DB 3; Length 3331;
Best Local Similarity 88.7%; Pred. No. 1.7e-48;
Matches 250; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 303 CTGCTTGGATTCCTTAGCACACACAGCTCAGCAGAACAGAGGCGCTCGAATCTCAT 362
Db 191 CCGCTTGGATTCCTCAGCACCATCACAGCTCAACAGAACAAAAGACTCTGTGAGTCTCCCT 250

QY 363 GGCACATACCGCATGTTGACCGTGCCACCGCCAGGTGCTAACCTGTGACAAAGTGCCA 422
Db 251 GGCACCTACCGCATGTTGACCGTGCCACCTGCGCCAGGTGCTAACCTGCGAACAGTGCCCA 310

QY 423 GCAGGAACCTATGTCTCTGAGCATTTGACCAACACAAAGCCTGCGCGTCTGCAGCAGTTGC 482
Db 311 GCAGGAACCTATGTCTCTCGAGCACTGTACCAACATGAGCCTGCGAGTCTGCAGCAGTTGC 370

QY 483 CTTGTGGGACCTTTACAGGATGAGAAATGGCATAGAGAAATGCCATGACTGTAGTCAG 542
Db 371 CCGCGGGGACCTTTACAGGACGACGAGACGCGCATAGAGATGCCATGACTGTAGTCAG 430

QY 543 CCATGCCCATGGCAATGATTGAAATACCTTGCTGCC 584
Db 431 CCATGTCCTGCGCGATGATTGAGAGATTACCTTGCTGCC 472

RESULT 15
US-09-016-434-652
; Sequence 652, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 652:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: HNT2RAT01
; CLONE: 260827
; US-09-016-434-652

Query Match 27.9%; Score 163.2; DB 4; Length 359;
Best Local Similarity 92.6%; Pred. No. 7.5e-32;
Matches 201; Conservative 0; Mismatches 13; Indels 3; Gaps 3;

QY 371 CCGCCATGTTGACCGTG-CCACCGCCAGGTGCTAACCTGTGACAAGTGTCCAGCAGGAA 429
Db 1 CCGCCATGTTGACCGTGACCCACCGCCAGGTGCTAACCTGTGACAAGTGTCCAGCAGGAA 60

QY 430 CCTATGCTCTGAGCATTTGACCAACACAAAGCCTGCGCGTCTGCAGCAGTTGCCCTGTGG 489
Db 61 CCTATGCTCTNAGCATTTGACCAACACAAAGCCTGCGCGTCTGCAGCAGTTGCCCTGTGG 120

QY 490 GGACCTTTTACCAGGCATGAGAAATGGCATAGAG-AAATGGCCATGACTGTAGTCAGCCATGC 548
Db 121 GGACCTTTTACCAGGCATGGGNGGCGCATAGAGTTTTTTTNCATGACTINTAGTCAGCCATGC 180

QY 549 CCATGSCCAATG-ATTGAGAAATTAACCTTGCTGCC 584
Db 181 CCATGSCCAATGAATTGAGAAATNACCTTGCTGCC 217

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 8, 2005, 02:56:22 ; Search time 571 Seconds
(without alignments)
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Title: US-10-663-157-3

Perfect score: 584

Sequence: 1 ggcncgcgmngngncaag.....agaattacctgtgtgtgcc 584

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 - 19: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
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 - 21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	578	99.0	584	17	US-10-663-157-3
2	550.2	94.2	588	17	Sequence 3, Appli
3	544.8	93.3	2877	9	Sequence 5, Appli
4	544.8	93.3	3474	9	Sequence 5, Appli
5	544.8	93.3	3474	13	Sequence 1, Appli
6	544.8	93.3	3474	18	Sequence 1, Appli
7	543.2	93.0	3534	9	Sequence 63, Appli
8	543.2	93.0	3534	9	Sequence 63, Appli
9	543.2	93.0	3534	9	Sequence 63, Appli
10	543.2	93.0	3534	9	Sequence 63, Appli
11	543.2	93.0	3534	10	Sequence 63, Appli
12	543.2	93.0	3534	10	Sequence 63, Appli

13	543.2	93.0	3534	10	US-09-978-585A-63	Sequence 63, Appli
14	543.2	93.0	3534	10	US-09-978-191A-63	Sequence 63, Appli
15	543.2	93.0	3534	10	US-09-978-403A-63	Sequence 63, Appli
16	543.2	93.0	3534	10	US-09-978-564A-63	Sequence 63, Appli
17	543.2	93.0	3534	10	US-09-999-833A-63	Sequence 63, Appli
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27	543.2	93.0	3534	10	US-09-978-187B-63	Sequence 63, Appli
28	543.2	93.0	3534	10	US-09-978-643A-63	Sequence 63, Appli
29	543.2	93.0	3534	10	US-09-978-375A-63	Sequence 63, Appli
30	543.2	93.0	3534	10	US-09-978-298A-63	Sequence 63, Appli
31	543.2	93.0	3534	10	US-09-978-188A-63	Sequence 63, Appli
32	543.2	93.0	3534	10	US-09-978-681A-63	Sequence 63, Appli
33	543.2	93.0	3534	10	US-09-978-194A-63	Sequence 63, Appli
34	543.2	93.0	3534	10	US-09-999-829A-63	Sequence 63, Appli
35	543.2	93.0	3534	10	US-09-978-299A-63	Sequence 63, Appli
36	543.2	93.0	3534	10	US-09-978-544A-63	Sequence 63, Appli
37	543.2	93.0	3534	10	US-09-978-802A-63	Sequence 63, Appli
38	543.2	93.0	3534	10	US-09-978-665A-63	Sequence 63, Appli
39	543.2	93.0	3534	13	US-10-052-586-417	Sequence 417, App
40	543.2	93.0	3534	14	US-10-174-590-417	Sequence 417, App
41	543.2	93.0	3534	14	US-10-176-758-417	Sequence 417, App
42	543.2	93.0	3534	14	US-10-175-737-417	Sequence 417, App
43	543.2	93.0	3534	14	US-10-174-581-417	Sequence 417, App
44	543.2	93.0	3534	14	US-10-176-483-417	Sequence 417, App
45	543.2	93.0	3534	14	US-10-176-749-417	Sequence 417, App

ALIGNMENTS

RESULT 1
US-10-663-157-3
; Sequence 3, Application US/10663157
; Publication No. US20040132057A1
; GENERAL INFORMATION:
; APPLICANT: DEEN, KEITH CHARLES
; APPLICANT: HURLE, MARK R.
; APPLICANT: YOUNG, PETER
; APPLICANT: TAN, K.B.
; TITLE OF INVENTION: DNA ENCODING TUMOR NECROSIS RELATED RECEPTOR TR7
; FILE REFERENCE: SKBG-3017US2
; CURRENT APPLICATION NUMBER: US/10/663,157
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/041,796
; PRIOR FILING DATE: 1997-04-02
; PRIOR APPLICATION NUMBER: US 08/959,382
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: US 09/314,844
; PRIOR FILING DATE: 1999-05-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 584
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (10)..(11)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature

LOCATION: (13)...(13)
OTHER INFORMATION: n is a, c, g, or t
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NAME/KEY: misc_feature
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OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (38)...(38)
OTHER INFORMATION: n is a, c, g, or t
US-10-663-157-3

Query Match 99.0%; Score 578; DB 17; Length 584;
Best Local Similarity 100.0%; Pred. No. 5e-154;
Matches 584; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GCGNCGCGNNGNGCAAGTGTCTAGAGCCCTTAGNGCCTCCCTTGGCGCTCCCTCC 60
QY 61 TCTGCCCGCGGTAGAGTGCACATGGGTGTTGGAGGTAGATGGGTCCCGCGCGGAG 120
DB 61 TCTGCCCGCGGTAGAGTGCACATGGGTGTTGGAGGTAGATGGGTCCCGCGCGGAG 120
QY 121 GCGCGGTGTAGTGGCGGTGGCGAGAGCAGCGCGCGGATTCAGCTGCGCGCGGCC 180
DB 121 GCGCGGTGTAGTGGCGGTGGCGAGAGCAGCGCGCGGATTCAGCTGCGCGCGGCC 180
QY 181 CGGCCACTTGGAGTCCCGGTTCAGCCATGGGACCTTCAGAGAGAGCAGCGGCC 240
DB 181 CGGCCACTTGGAGTCCCGGTTCAGCCATGGGACCTTCAGAGAGAGCAGCGGCC 240
QY 241 TCGCCTCTCGACCGCATGCGCGCGCGCGAGCAGCGAGTATCCAGATGCGGGGCTCCCTTC 300
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QY 301 TCTGTCTGTGATTCCTTAGCACACACACAGCTCAGCCAGAAACAGAGGCTCGAATCTCA 360
DB 301 TCTGTCTGTGATTCCTTAGCACACACACAGCTCAGCCAGAAACAGAGGCTCGAATCTCA 360
QY 361 TTGGCACAATACCGCATGTTGACCGTCCACCGCGAGGTGTAACCTGTGACAAATGTC 420
DB 361 TTGGCACAATACCGCATGTTGACCGTCCACCGCGAGGTGTAACCTGTGACAAATGTC 420
QY 421 CAGCAGAACTATGTCTGAGCATGTACCAACACAGCTGCGCGTCTGAGCAGTT 480
DB 421 CAGCAGAACTATGTCTGAGCATGTACCAACACAGCTGCGCGTCTGAGCAGTT 480
QY 481 GCGCTGTGGGACCTTTACAGGCATGAGAAATGCGCATAGAGAAATGCCATGACTGTAGTC 540
DB 481 GCGCTGTGGGACCTTTACAGGCATGAGAAATGCGCATAGAGAAATGCCATGACTGTAGTC 540
QY 541 AGCCATGCCATGGCAATGTTGAGAAATTAACCTTGTGTGTC 584
DB 541 AGCCATGCCATGGCAATGTTGAGAAATTAACCTTGTGTGTC 584

RESULT 2

US-10-663-157-5
Sequence 5, Application US/10663157
Publication No. US20040132057A1
GENERAL INFORMATION:
APPLICANT: DEEN, KEITH CHARLES
APPLICANT: HURLE, MARK R.
APPLICANT: YOUNG, PETER
APPLICANT: TAN, K.B.
FILE OF INVENTION: DNA ENCODING TUMOR NECROSIS RELATED RECEPTOR TR7
CURRENT FILING DATE: 2003-09-15
CURRENT APPLICATION NUMBER: US/10/663,157
PRIOR FILING DATE: 1997-04-02
PRIOR APPLICATION NUMBER: US 08/959,382

PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: US 09/314,844
PRIOR FILING DATE: 1999-05-19
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patent in version 3.2
SEQ ID NO 5
LENGTH: 588
TYPE: DNA
ORGANISM: HOMO SAPIENS
FEATURE:
NAME/KEY: misc_feature
LOCATION: (4)...(4)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (10)...(11)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (13)...(13)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (15)...(15)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (38)...(38)
OTHER INFORMATION: n is a, c, g, or t
US-10-663-157-5

Query Match 94.2%; Score 550.2; DB 17; Length 588;

Best Local Similarity 98.5%; Pred. No. 3.9e-146;
Matches 572; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

QY 1 GCGNCGCGNNGNGCAAGTGTCTAGAGCCCTTAGNGCCTCCCTTGGCGCTCCCTCC 60
DB 1 GCGNCGCGNNGNGCAAGTGTCTAGAGCCCTTAGNGCCTCCCTTGGCGCTCCCTCC 60
QY 61 TCTGCCCGCGGTAGAGTGCACATGGGTGTTGGAGGTAGATGGGTCCCGCGCGGAG 120
DB 61 TCTGCCCGCGGTAGAGTGCACATGGGTGTTGGAGGTAGATGGGTCCCGCGCGGAG 120
QY 121 GCGCGGTGTAGTGGCGGTGGCGAGAGCAGCGCGGATTCAGCTGCGCGCGGCC 180
DB 121 GCGCGGTGTAGTGGCGGTGGCGAGAGCAGCGCGGATTCAGCTGCGCGCGGCC 180
QY 181 CGGCCACTTGGAGTCCCGGTTCAGCCATGGGACCTTCAGAGAGAGCAGCGGCC 240
DB 181 CGGCCACTTGGAGTCCCGGTTCAGCCATGGGACCTTCAGAGAGAGCAGCGGCC 240
QY 241 TC-GCTCTCTGAGCGGCATCGCCCGCGAGCAGCAGCATGATCGCGGCTCCCTT 299
DB 241 TCGGCTCTCTGCAACCGCATCGCCCGCGAGCAGCAGCATGATCGCGGCTCCCTT 300
QY 300 CTCCTGTGTGATTCCTTAGCACACACAGCTCAGCCAGAAACAGAGGCTCGAATCTC 359
DB 301 CTCCTGTGTGATTCCTTAGCACACACAGCTCAGCCAGAAACAGAGGCTCGAATCTC 360
QY 360 ATTGGCACAATACCGCATGTTGACCGTGCACCGCGCGAGGTGCTAACCTGTGACAGTGT 419
DB 361 ATTGGCACAATACCGCATGTTGACCGTGCACCGCGCGAGGTGCTAACCTGTGACAGTGT 420
QY 420 CCAGAGGAGAACCTATGTCTCTGAGCATGTGTACCAACAGAGGCTCGGCTCTGTCAGCAGT 479
DB 421 CCAGAGGAGAACCTATGTCTCTGAGCATGTGTACCAACAGAGGCTCGGCTCTGTCAGCAG 480
QY 480 TCGCCTGTGGGACCTTTACAGGCATGAGAAATGCGCATAGAGAAATGCCATGACTGTAGT 539
DB 481 TCGCCTGTGGGACCTTTACAGGCATGAGAAATGCGCATAGAGAAATGCCATGACTGTAGT 540
QY 540 CAGCATGCCATGCCCAATGATTGAGAAATTAACCTTGTGTC 580

Db 541 CAGCCATGCCATGGCCCAATGATTGAGAAATTACCTTGTGCC 581

RESULT 3

US-09-840-795-5
; Sequence 5, Application US/09840795
; Patent No. US20020143147A1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Erin E.
; APPLICANT: Mattson, Jeanine D.
; APPLICANT: Bates, Elizabeth Esther Mary
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Lebecque, Serge J.E.
; TITLE OF INVENTION: Mammalian Genes; Related Reagents
; FILE REFERENCE: SF0818K
; CURRENT APPLICATION NUMBER: US/09/840,795
; CURRENT FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: 09/351,777
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 2877
; TYPE: DNA
; ORGANISM: primate
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (410)..(2374)
; NAME/KEY: mat_peptide
; LOCATION: (533)..(2374)
US-09-840-795-5

Query Match 93.3%; Score 544.8; DB 9; Length 2877;
Best Local Similarity 97.4%; Pred. No. 1.5e-144;
Matches 571; Conservative 0; Mismatches 13; Indels 2; Gaps 2;
QY 1 GCGNCCGCGNNGNGCAAGGTCTGAGCGCCCTAGNGCTCCTCCCTTGGCGCTCCCTCC 60
Db 199 GCGGCGCGCGCTGGGCGAGTGTGAGCGCCCTAGCGCTCCTTGGCGCTCCCTCC 258
QY 61 TCTGCCCGCGGTAGCAGTGCATGGGGTGTGGAGTAGAGTGGCTCCCGG-CCGGGA 119
Db 259 TCTGCCCGCGCGAGCAGTGCATGGGGTGTGGAGTAGAGTGGCTCCCGGCGCGGA 318
QY 120 GCGGCGCGGTGGTGGCGCGTGGGCAAGCAGCGCGGATTCAGCTGCCCGCGCGCC 179
Db 319 GCGGCGCGGTGGTGGCGCGTGGGCAAGCAGCGCGGATTCAGCTGCCCGCGCGCC 378
QY 180 CC-GGCCACCTTGGAGTCCCGGTTCCAGCATGGGGACCTCTCCGAGCAGCAGCCGC 238
Db 379 CCGGCGCGCTGCGAGTCCCGGTTCCAGCATGGGGACCTCTCCGAGCAGCAGCCGC 438
QY 239 CTTGCGCTCTGAGCGCGATCGCCCGCGAGCCAGCCAGCATGATCGGGCTCCCT 298
Db 439 CTTGCGCTCTGAGCGCGATCGCCCGCGAGCCAGCCAGCATGATCGGGCTCCCT 498
QY 299 TCTCTCTCTTGGATTCTTAGCACCACACAGCTCAGCCAGAACAGAAAGCCTCGAATCT 358
Db 499 TCTCTCTCTTGGATTCTTAGCACCACACAGCTCAGCCAGAACAGAAAGCCTCGAATCT 558
QY 359 CATTTGGCACATACCGCATGTTGACCGTGCACCGCGAGGTGCTAACCTGTGACAGTG 418
Db 559 CATTTGGCACATACCGCATGTTGACCGTGCACCGCGAGGTGCTAACCTGTGACAGTG 618
QY 419 TCCAGCAGGAACCTATGTTCTTAGGATTGTATCCAAACAGCGCTGGCGCTTGCAGCAG 478
Db 619 TCCAGCAGGAACCTATGTTCTTAGGATTGTATCCAAACAGCGCTGGCGCTTGCAGCAG 678
QY 479 TTGCGCTGTGGGACCTTTTACCAGGCATGAGATGGCATAGAGAAATGCCATGACTGTAG 538
Db 679 TTGCGCTGTGGGACCTTTTACCAGGCATGAGATGGCATAGAGAAATGCCATGACTGTAG 738
QY 539 TCAGCCATGCCCATGGCCAAATGATTGAGAAATTACCTTGTGTGCC 584

Db 739 TCAGCCATGCCATGCCCAATGATTGAGAAATTACCTTGTGTGCC 784

RESULT 4

US-09-756-854-1
; Sequence 1, Application US/09756854
; Patent No. US20020164684A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Fan, Ping
; APPLICANT: Gentz, Reiner
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/756,854
; FILING DATE: 10-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/095,094
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoover, Kenley K.
; REGISTRATION NUMBER: 40,302
; REFERENCE/DOCKET NUMBER: PF375
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3474 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 247..2211
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 367..2211
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 247..364
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-756-854-1

Query Match 93.3%; Score 544.8; DB 9; Length 3474;
Best Local Similarity 97.4%; Pred. No. 1.6e-144;
Matches 571; Conservative 0; Mismatches 13; Indels 2; Gaps 2;
QY 1 GCGNCCGCGNNGNGCAAGGTCTGAGCGCCCTAGNGCTCCTTGGCGCTCCCTCC 60
Db 36 GCGGCGCGCGCTGGGCGAGTGTGAGCGCCCTAGAGCTCCTTGGCGCTCCCTCC 95
QY 61 TCTGCCCGCGGTAGCAGTGCATGGGGTGTGGAGTAGAGTGGCTCCCGG-CCGGGA 119
Db 96 TCTGCCCGCGCGAGCAGTGCATGGGGTGTGGAGTAGAGTGGCTCCCGGCGCGGA 155
QY 120 GCGGCGCGGTGGATGCGGCGCTGGGCGAGCAGCCGCGATTCAGCTGCCCGCGGCC 179

Db 156 GCGCGCGGTGGATGCGCGCGTGGGCAAGCAGCCGCCGATTCAGCTGCCCGCGCC 215
QY 180 CC-GGCACCTTGGAGTCCCGGTTCAGCCATGGGAGCTCTCCGAGCAGCAGCAGC 238
Db 216 CCGGCGCGCCCTGCGAGTCCCGGTTCAGCCATGGGAGCTCTCCGAGCAGCAGCAGC 275
QY 239 CTTGCGCTCTGAGCGCGCATGCGCGCGCGAGCCACAGCCAGCATGATCGCGGCTCCCT 298
Db 276 CTTGCGCTCTGAGCGCGCATGCGCGCGCGAGCCACAGCCAGCATGATCGCGGCTCCCT 335
QY 299 TCTCTGCTTGGATTCCTTAGCACCACACAGCTCAGCCAGAAACAGAGGCTCGAATCT 358
Db 336 TCTCTGCTTGGATTCCTTAGCACCACACAGCTCAGCCAGAAACAGAGGCTCGAATCT 395
QY 359 CATTGGCACATACCGGCATGTTACCGTGCACCGCGCAGGTGTAACCTGTGACAAGTG 418
Db 396 CATTGGCACATACCGGCATGTTACCGTGCACCGCGCAGGTGTAACCTGTGACAAGTG 455
QY 419 TCCAGCAGGAACCTATGCTCTGAGCATTTACCAACAGGCTGCGGTCTGCGAGCAG 478
Db 456 TCCAGCAGGAACCTATGCTCTGAGCATTTACCAACAGGCTGCGGTCTGCGAGCAG 515
QY 479 TTGCGCTGTGGGACCTTTACAGGCGATGAGAAATGGCATAGAGAAATGCGAGTGTAG 538
Db 516 TTGCGCTGTGGGACCTTTACAGGCGATGAGAAATGGCATAGAGAAATGCGAGTGTAG 575
QY 539 TCAGCCATGCCCATGCCAATGATTGAGAAATTTACCTTTGTGTGCC 584
Db 576 TCAGCCATGCCCATGCCAATGATTGAGAAATTTACCTTTGTGTGCC 621

RESULT 5

US-10-041-574-1
; Sequence 1, Application US/10041574
; Publication No. US20020168359A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Fan, Ping
; APPLICANT: Gentz, Reiner L.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
; FILE REFERENCE: PF375P1
; CURRENT APPLICATION NUMBER: US/10/041,574
; CURRENT FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: 09/527,236
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/052,991
; PRIOR FILING DATE: 1997-06-11
; PRIOR APPLICATION NUMBER: 09/095,094
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/126,019
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: 60/134,220
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3474
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (247)..(2211)
; NAME/KEY: sig_peptide
; LOCATION: (247)..(366)
; NAME/KEY: mat_peptide
; LOCATION: (367)..(2211)

US-10-041-574-1

Query Match 93.3%; Score 544.8; DB 13; Length 3474;
Best Local Similarity 97.4%; Pred. No. 1.6e-144;
Matches 571; Conservative 0; Mismatches 13; Indels 2; Gaps 2;

QY 1 GCGNCCGNGNGNGCAAGGTGCTGAGCGCCCTAGNGCCTCCCTTGGCGGCTCCCTCC 60
Db 36 GCGGCGCGCCCGCTGGGCAAGTGTGAGCGCCCTAGAGCCTCCCTTGGCGGCTCCCTCC 95
QY 61 TCTGCGCGCGCTAGCAGTGCACATGCGGTGTGGAGGTAGATGGGCTCCCGG-CCGGGA 119
Db 96 TCTGCGCGCGCGCAGCAGTGCACATGCGGTGTGGAGGTAGATGGGCTCCCGGCGCGGA 155
QY 120 GCGGCGGTGGATGCGGCGCTGGGCAAGCAGCGCCGATTCAGCTCCCGCGCGCCG 179
Db 156 GCGGCGGTGGATGCGGCGCTGGGCAAGCAGCGCCGATTCAGCTCCCGCGCGCCG 215
QY 180 CC-GGCACCTTGGAGTCCCGGTTCAGCCATGGGAGCTCTCCGAGCAGCAGCAGC 238
Db 216 CCGGCGCGCCCTGCGAGTCCCGGTTCAGCCATGGGAGCTCTCCGAGCAGCAGCAGC 275
QY 239 CTTGCGCTCTGAGCGCGCATGCGCGCGCGAGCCACAGCATGATCGCGGCTCCCT 298
Db 276 CTTGCGCTCTGAGCGCGCATGCGCGCGCGAGCCACAGCATGATCGCGGCTCCCT 335
QY 299 TCTCTGCTTGGATTCCTTAGCACCACACAGCTCAGCCAGAAACAGAGGCTCGAATCT 358
Db 336 TCTCTGCTTGGATTCCTTAGCACCACACAGCTCAGCCAGAAACAGAGGCTCGAATCT 395
QY 359 CATTGGCACATACCGGCATGTTACCGTGCACCGCGCAGGTGTAACCTGTGACAAGTG 418
Db 396 CATTGGCACATACCGGCATGTTACCGTGCACCGCGCAGGTGTAACCTGTGACAAGTG 455
QY 419 TCCAGCAGGAACCTATGCTCTGAGCATTTACCAACAGGCTGCGGTCTGCGAGCAG 478
Db 456 TCCAGCAGGAACCTATGCTCTGAGCATTTACCAACAGGCTGCGGTCTGCGAGCAG 515
QY 479 TTGCGCTGTGGGACCTTTACAGGCGATGAGAAATGGCATAGAGAAATGCGAGTGTAG 538
Db 516 TTGCGCTGTGGGACCTTTACAGGCGATGAGAAATGGCATAGAGAAATGCGAGTGTAG 575
QY 539 TCAGCCATGCCCATGCCAATGATTGAGAAATTTACCTTTGTGTGCC 584
Db 576 TCAGCCATGCCCATGCCAATGATTGAGAAATTTACCTTTGTGTGCC 621

RESULT 6

US-10-834-966-1
; Sequence 1, Application US/10834966
; Publication No. US20040197870A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Fan, Ping
; APPLICANT: Gentz, Reiner L.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
; FILE REFERENCE: PF375P1
; CURRENT APPLICATION NUMBER: US/10/834,966
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: US/10/041,574
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: 09/527,236
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/052,991
; PRIOR FILING DATE: 1997-06-11
; PRIOR APPLICATION NUMBER: 09/095,094
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/126,019
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: 60/134,220
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3474
; TYPE: DNA
; ORGANISM: Homo sapiens

FEATURE:
; NAME/KEY: CDS
; LOCATION: (247) .. (2211)
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (247) .. (366)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (367) .. (2211)
US-10-834-966-1

Query Match 93.38; Score 544.8; DB 18; Length 3474;
Best Local Similarity 97.44; Pred. No. 1.6e-144;
Matches 571; Conservative 0; Mismatches 13; Indels 2; Gaps 2;
QY 1 GCGNCCGCGGNGNGCAAGTGTCTGAGCGCCCTCTAGNGCCTCCCTTGGCGCTCCCTCC 60
Db |||||
QY 61 TCTGCCCGCGGTAGCAGTGCACATGGGGTGTGGAGGTAGATGGCTCCCG-CCGGGA 119
Db |||||
QY 96 TCTGCCCGCGCGAGCAGTGCACATGGGGTGTGGAGGTAGATGGCTCCCGCCGGGA 155
Db |||||
QY 120 GCGGGCGGTGATGCGCGCTGGGCAGACAGCGCCGATTCAGTGTCCCGCGCGCC 179
Db |||||
QY 156 GCGGGCGGTGATGCGCGCTGGGCAGACAGCGCCGATTCAGTGTCCCGCGCGCC 215
Db |||||
QY 180 CC-GGCCACCTTGGAGTCCCGGTTCCAGCCATGGGGACCTCTCCGAGCAGACGCCG 238
Db |||||
QY 216 CCGGGCGCCCTGGAGTCCCGGTTCCAGCCATGGGGACCTCTCCGAGCAGACGCCG 275
Db |||||
QY 239 CTTGCGCTCTGAGCGCGCATCGCCCGGAGCCACAGCCAGCATGATCGCGGCTCCCT 298
Db |||||
QY 276 CTTGCGCTCTGAGCGCGCATCGCCCGGAGCCACAGCCAGCATGATCGCGGCTCCCT 335
Db |||||
QY 299 TCTCTGCTTGGATTCTTACGACCCACAGCTCAGCCAGAAACAGAGGCTTCGAATCT 358
Db |||||
QY 336 TCTCTGCTTGGATTCTTACGACCCACAGCTCAGCCAGAAACAGAGGCTTCGAATCT 395
Db |||||
QY 359 CATTTGGCACATACCGCATCTTACCGTCCCGGAGGCTTACCTGTGCACAGTG 418
Db |||||
QY 396 CATTTGGCACATACCGCATCTTACCGTCCCGGAGGCTTACCTGTGCACAGTG 455
Db |||||
QY 419 TCCAGCAGGAACCTATCTCTGAGCATTTGACACACAGGCTGCGGCTGTGCACAG 478
Db |||||
QY 456 TCCAGCAGGAACCTATCTCTGAGCATTTGACACACAGGCTGCGGCTGTGCACAG 515
Db |||||
QY 479 TTGCGCTGTGGGACCTTTTACCGGCAATGAGATGGCATAGAGAAATGCCATGCTGAG 538
Db |||||
QY 516 TTGCGCTGTGGGACCTTTTACCGGCAATGAGATGGCATAGAGAAATGCCATGCTGAG 575
Db |||||
QY 539 TCAGCCATGCCATGCCCAATGATTTGAGAAATACCTTGTGCTGCC 584
Db |||||
QY 576 TCAGCCATGCCATGCCCAATGATTTGAGAAATACCTTGTGCTGCC 621
Db |||||

RESULT 7

US-09-978-295A-63
; Sequence 63, Application US/09978295A
; Patent No. US20020156006A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC11
CURRENT APPLICATION NUMBER: US/09/978,295A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079663
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079786
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079920
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/079923
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/080105
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080107
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080165

;
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080194
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080327
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080328
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080333
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080334
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/081070
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081049
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081071
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081195
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081203
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081229
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081817
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081952
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081838
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082568
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082569
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082704
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082700
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082797
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082796
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: 60/083336
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/083392
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083495
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083496
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 93.0%; Score 543.2; DB 9; Length 3534;
Best Local Similarity 97.3%; Pred. No. 4.4e-144;
Matches 570; Conservative 0; Mismatches 14; Indels 2; Gaps 2;

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DB 174 TCTGCCCGCGCGCAGCAGTGACATGGGGTGTGGAGGTAGATGGCTCCCGGCGGGA 233
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RESULT 8

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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Flvaroff, Ellen
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; APPLICANT: Paoni, Nicholas F.
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; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C27
; CURRENT APPLICATION NUMBER: US/09/978,697
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; PRIOR APPLICATION NUMBER: 09/918585
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;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 93.0%; Score 543.2; DB 9; Length 3534;
Best Local Similarity 97.3%; Pred. No. 4.4e-144;
Matches 570; Conservative 0; Mismatches 14; Indels 2; Gaps 2;

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QY 539 TCAGCATGCCCATGCCCAATGATTGAGAAATTTACCTTTGTGTGCTGCC 584
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RESULT 9
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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
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; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
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; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.

;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2630P1C9

;; CURRENT FILING DATE: 2001-10-15

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Query Match 93.0%; Score 543.2; DB 9; Length 3534;

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Matches 570; Conservative 0; Mismatches 14; Indels 2; Gaps 2;

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QY 299 TCTCTGCTTGGATTCTTAGCACCACACAGCTCAGCCAGCAAGCAAGCCCTCGAATCT 358
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QY 359 CATTTGCACATACCGCCATGTTGACCGTGCCACCGCGCGAGTGTAACTGTGACAAGTG 418
Db 474 CATTTGCACATACCGCCATGTTGACCGTGCCACCGCGCGAGTGTAACTGTGACAAGTG 533
QY 419 TCAGCAGGAACCTATGTTCTGAGCAATTTGTAACAACAAGCCTCGCGTCTGCAAGCAG 478
Db 534 TCAGCAGGAACCTATGTTCTGAGCAATTTGTAACAACAAGCCTCGCGTCTGCAAGCAG 593
QY 479 TTGCGCTTGGGACCTTTTACCAGGATGAGATGGCATAGAAATGCCATGACTGTAG 538
Db 594 TTGCGCTTGGGACCTTTTACCAGGATGAGATGGCATAGAAATGCCATGACTGTAG 653
QY 539 TCAGCCATGCCATGCCCAATGATTGAGAAATACCTTGTGTGCC 584
Db 654 TCAGCCATGCCATGCCCAATGATTGAGAAATACCTTGTGTGCC 699

RESULT 10

US-09-999-832A-63

; Sequence 63, Application US/09999832A

Publication No. US20020192706A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC63
CURRENT APPLICATION NUMBER: US/09/999,832A
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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; PRIOR FILING DATE: 1998-05-15
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 93.0%; Score 543.2; DB 9; Length 3534;

Best Local Similarity 97.3%; Pred. No. 4.4e-144;

Matches 570; Conservative 0; Mismatches 14; Indels 2; Gaps 2;

QY 1 GCGNCCGCGNNGNCAAGGTGCTGAGCGCCCTTAGNGCCTTCCCTTGGCGCTCCCTCC 60

Db 114 GCGGCTCGCGGCTGGGCGAGTGCTGAGCGCCCTTAGAGCTCCCTTGGCGCTCCCTCC 173

QY 61 TCTGCCGCGCGCTAGCAGTGCCATGGGCTGTTGGAGGTAGATGGGCTCCCGG-CCGGGA 119

Db 174 TCTGCCGCGCGCGCAGCAGTGCCATGGGCTGTTGGAGGTAGATGGGCTCCCGGCGCGGA 233

QY 120 GCGGCGGCTGGATGCGGCGCTGGGCGAAGACGCCCGGATTCAGCTGCCCGCGCGCC 179

Db 234 GCGGCGGCTGGATGCGGCGCTGGGCGAAGACGCCCGGATTCAGCTGCCCGCGCGCC 293

QY 180 CC-GGCCACCTTCGAGTCCCGGTTTCAGCCATGGGGACCTTCCGAGCAGCAGCACCGC 238

Db 294 CCGGCGCGCCCTTCGAGTCCCGGTTTCAGCCATGGGGACCTTCCGAGCAGCAGCACCGC 353

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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 93.0%; Score 543.2; DB 10; Length 3534;
Best Local Similarity 97.3%; Pred. No. 4.4e-144;
Matches 570; Conservative 0; Mismatches 14; Indels 2; Gaps 2;

QY 1 GCGNCGCGNNGNGCAAGGTGCTGAGCGCCCTAGNCGCTCCCTTGGCGCCTCCCTCC 60
DB 114 GCGGCTTCCGCGCTGGGAGGTGCTGAGCGCCCTAGAGCCTCCCTTGGCGCCTCCCTCC 173
QY 61 TCTGCCCGCGCTGAGTGCACATGGGGTGTGGAGGTAGATGGGCTCCCGG-CCGGGA 119
DB 174 TCTGCCCGCGCGCAGCAGTGCACATGGGGTGTGGAGGTAGATGGGCTCCCGGCCGGGA 233
QY 120 GCGGCGGTGGATGCGCGCTGGGAGAGCAGCGCCGATTCACGCTGCCCGCGGCC 179
DB 234 GCGGCGGTGGATGCGCGCTGGGAGAGCAGCGCCGATTCACGCTGCCCGCGGCC 293
QY 180 CC-GGCGACCTTCGCGAGTCCCGGTTTCAGCCATGGGGACCTCTCCGAGCAGCAGCACCGC 238
DB 294 CCGGCGCGCTTCGCGAGTCCCGGTTTCAGCCATGGGGACCTCTCCGAGCAGCAGCACCGC 353
QY 239 CTTTCGCTCTGCGAGCGCATGCGCGCGAGCCACAGCCACGATGATCGCGGCTCCCT 298
DB 354 CTTTCGCTCTGCGAGCGCATGCGCGCGAGCCACAGCCACGATGATCGCGGCTCCCT 413
QY 299 TCTCTGCTTGGATTCTTTAGCACACACAGCTCAGCCAGCAGAGCCCTCGAATCT 358
DB 414 TCTCTGCTTGGATTCTTTAGCACACACAGCTCAGCCAGCAGAGCCCTCGAATCT 473
QY 359 CATTTGCACATACCGCATGTTGACCGTGCCACCGCGCAGGTCTTAACCTGTGACAAGTG 418
DB 474 CATTTGCACATACCGCATGTTGACCGTGCCACCGCGCAGGTCTTAACCTGTGACAAGTG 533
QY 419 TCCAGCAGGAACCTATGTTCTTGAGCATTGTACCAACACAAGCCTCGCGCTTGCAGCAG 478
DB 534 TCCAGCAGGAACCTATGTTCTTGAGCATTGTACCAACACAAGCCTCGCGCTTGCAGCAG 593
QY 479 TTGCCCTGTGGGACCTTTTACCAGGATGAGATGAGAAATGCCATGACTGTAG 538
DB 594 TTGCCCTGTGGGACCTTTTACCAGGATGAGATGAGAAATGCCATGACTGTAG 653
QY 539 TCAGCCATGCCCATGCCAATGATTGAGAAATTTACCTTTGTGTGCC 584
DB 654 TCAGCCATGCCCATGCCAATGATTGAGAAATTTACCTTTGTGTGCC 699

RESULT 12
US-09-978-608A-63
; Sequence 63, Application US/09978608A
; Publication No. US20030045462A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.

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/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Hillan, Kenneth J.
/ APPLICANT: Kljavin, Ivar J.
/ APPLICANT: Kuo, Sophia S.
/ APPLICANT: Napier, Mary A.
/ APPLICANT: Pan, James;
/ APPLICANT: Paoni, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Shelton, David L.
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William I.
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ FILE REFERENCE: P2630P1C22
/ CURRENT APPLICATION NUMBER: US/09/978,608A
/ CURRENT FILING DATE: 2001-10-16
/ NUMBER OF SEQ ID NOS: 624
/ Prior Application removed - See File Wrapper or Palm
/ SEQ ID NO 63
/ LENGTH: 3534
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-978-608A-63

Query Match          93.0%; Score 543.2; DB 10; Length 3534;
Best Local Similarity 97.3%; Pred. No. 4.4e-144;
Matches 570; Conservative 0; Mismatches 14; Indels 2; Gaps 2;

QY 1 GCGNCCGCGNNGNGCAAGGTGCTGAGCGCCCTAGNGCCTCCCTTGGCGCTCCCTCC 60
Db 114 GCGGCTCGCCGCTGGCAGGTGCTGAGCGCCCTAGAGCTCCCTTGGCGCTCCCTCC 173
QY 61 TCTGCCCGCGCTGAGCAGTGCACATGGGGTGTGGAGGTAGATGGGCTCCCGG 119
Db 174 TCTGCCCGCGCGCAGCAGTGCACATGGGGTGTGGAGGTAGATGGGCTCCCGCGGGA 233
QY 120 GCGCGGGTGGATGCGCGCTGGCAGAGCAGCGCCGATTCAGCTGCGCGCGCC 179
Db 234 GCGCGGGTGGATGCGCGCTGGCAGAGCAGCGCCGATTCAGCTGCGCGCGCC 293
QY 180 CC-GGCGACCTTCGAGTCCCGGTTCCAGCATGGGGACCTCCGAGCAGCAGCAGCCG 238
Db 294 CCGGGCGCCCTCGAGTCCCGGTTCCAGCATGGGGACCTCCGAGCAGCAGCAGCCG 353
QY 239 CTTGCGCTCTGTCAGCGCATGCGCGCGCAGCCAGCCAGCATGATCGCGGCTCCCT 298
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QY 299 TCTCCTGCTTGGATTCCTTAGCACCACAGCAGCTCAGCCAGCAGAGGCTCGAATCT 358
Db 414 TCTCCTGCTTGGATTCCTTAGCACCACAGCAGCTCAGCCAGCAGAGGCTCGAATCT 473
QY 359 CATTTGCACATACCGGCATGTTGACCGTGCCAGCGCAGGTCTAACCTGTGCAAGTG 418
Db 474 CATTTGCACATACCGGCATGTTGACCGTGCCAGCGCAGGTCTAACCTGTGCAAGTG 533
QY 419 TCCAGCAGGAACCTATGTCTCTGAGATTGTACCAACACAAGCTCGGCTGTGACGAG 478
Db 534 TCCAGCAGGAACCTATGTCTCTGAGATTGTACCAACACAAGCTCGGCTGTGACGAG 593
QY 479 TTGCGCTGTGGGACCTTTACAGGATGAGATGCGATAGAGAAATGCCATGACTGTAG 538
Db 594 TTGCGCTGTGGGACCTTTACAGGATGAGATGCGATAGAGAAATGCCATGACTGTAG 653
QY 539 TCAGCCATGCCATGCCAATGATGAGAAATACCTTTGTGCTGCC 584
Db 654 TCAGCCATGCCATGCCAATGATGAGAAATACCTTTGTGCTGCC 699
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RESULT 13

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US-09-978-585A-63
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/ GENERAL INFORMATION:
/ APPLICANT: Ashkenazi, Avi
/ APPLICANT: Baker Kevin P.
/ APPLICANT: Botstein, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Eaton, Dan
/ APPLICANT: Ferrara, Napoleon
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gao, Wei-Qiang
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/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Hillan, Kenneth J.
/ APPLICANT: Kljavin, Ivar J.
/ APPLICANT: Kuo, Sophia S.
/ APPLICANT: Napier, Mary A.
/ APPLICANT: Pan, James;
/ APPLICANT: Paoni, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Shelton, David L.
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William I.
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ FILE REFERENCE: P2630P1C15
/ CURRENT APPLICATION NUMBER: US/09/978,585A
/ CURRENT FILING DATE: 2001-10-16
/ NUMBER OF SEQ ID NOS: 624
/ Prior Application removed - See File Wrapper or Palm
/ SEQ ID NO 53
/ LENGTH: 3534
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-978-585A-63
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Query Match          93.0%; Score 543.2; DB 10; Length 3534;
Best Local Similarity 97.3%; Pred. No. 4.4e-144;
Matches 570; Conservative 0; Mismatches 14; Indels 2; Gaps 2;

QY 1 GCGNCCGCGNNGNGCAAGGTGCTGAGCGCCCTAGNGCCTCCCTTGGCGCTCCCTCC 60
Db 114 GCGGCTCGCCGCTGGCAGGTGCTGAGCGCCCTAGAGCTCCCTTGGCGCTCCCTCC 173
QY 61 TCTGCCCGCGCTGAGCAGTGCACATGGGGTGTGGAGGTAGATGGGCTCCCGG 119
Db 174 TCTGCCCGCGCGCAGCAGTGCACATGGGGTGTGGAGGTAGATGGGCTCCCGCGGGA 233
QY 120 GCGCGGGTGGATGCGCGCTGGCAGAGCAGCGCCGATTCAGCTGCGCGCGCC 179
Db 234 GCGCGGGTGGATGCGCGCTGGCAGAGCAGCGCCGATTCAGCTGCGCGCGCC 293
QY 180 CC-GGCGACCTTCGAGTCCCGGTTCCAGCATGGGGACCTCCGAGCAGCAGCAGCCG 238
Db 294 CCGGGCGCCCTCGAGTCCCGGTTCCAGCATGGGGACCTCCGAGCAGCAGCAGCCG 353
QY 239 CTTGCGCTCTGTCAGCGCATGCGCGCGCAGCCAGCCAGCATGATCGCGGCTCCCT 298
Db 354 CTTGCGCTCTGTCAGCGCATGCGCGCGCAGCCAGCCAGCATGATCGCGGCTCCCT 413
QY 299 TCTCCTGCTTGGATTCCTTAGCACCACAGCAGCTCAGCCAGCAGAGGCTCGAATCT 358
Db 414 TCTCCTGCTTGGATTCCTTAGCACCACAGCAGCTCAGCCAGCAGAGGCTCGAATCT 473
QY 359 CATTTGCACATACCGGCATGTTGACCGTGCCAGCGCAGGTCTAACCTGTGCAAGTG 418
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Db      474  CATTGGCACATACCGCCATGTTGACCGTGCCACCGCCAGGTGCTACCTGTGACAAGTG 533
Qy      419  TCAGCAGGAACTATCTCTGAGCATTTGACCAACAAGCTGGCGTCTGCAGCAG 478
Db      534  TCAGCAGGAACTATGTTCTGAGCATTTGACCAACAAGCTGGCGTCTGCAGCAG 593
Qy      479  TTGCGCTGTGGGACCTTTACCAAGGCATGAGAAATGGCATAGAGAAATGCCACTGTAG 538
Db      594  TTGCGCTGTGGGACCTTTACCAAGGCATGAGAAATGGCATAGAGAAATGCCACTGTAG 653
Qy      539  TCAGCCATGCCCATGGCCATGATTGAGAAATACCTTTGCTGCC 584
Db      654  TCAGCCATGCCCATGGCCATGATTGAGAAATACCTTTGCTGCC 699

RESULT 14
US-09-978-191A-63
; Sequence 63, Application US/09978191A
; Publication No. US20030050239A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnuyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
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; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
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; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
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Query Match 93.0%; Score 543.2; DB 10; Length 3534;
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Db 174 TCTGCCCGCGCGCAGCAGTGCATGGGGTGTGTGAGGTAGATGGCTCCCGCGCGGA 233

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Db 234 GCGCGGGTGGATGCGGGCTGGGCGAGAGCAGCCGCGATTCCAGCTGCCCGCGCGCC 293

QY 180 CC-GGCCACCTTTCGAGTCCCGGTTTCAGCCATGGGGACCTTCCGAGCAGCAGCCGC 238
Db 294 CCGGGCGCCCTTCGAGTCCCGGTTTCAGCCATGGGGACCTTCCGAGCAGCAGCCGC 353

QY 239 CTTGCTCTCTGAGCGCGCATCGCCGCGAGCCAGCCAGCAGTATCGCGGCTCCCT 298
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QY 299 TCTCTGCTTGGATTCTTAGCACCAACAGCTCAGCCAGAACAGAGGCTCGAATCT 358
Db 414 TCTCTGCTTGGATTCTTAGCACCAACAGCTCAGCCAGAACAGAGGCTCGAATCT 473

QY 359 CATTGGCAGATACCGCCATGTTGACCGTGCCACCGCCAGGTGCTAACTGTGACAGTG 418
Db 474 CATTGGCAGATACCGCCATGTTGACCGTGCCACCGCCAGGTGCTAACTGTGACAGTG 533

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Db 534 TCCAGCAGGAGCTATGTTCTGAGCATTGTACCAACAGCCCTGCGGCTCTGCAGCAG 593

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QY 539 TCAGCCATGCCCATGGCCAAATGATTGAGAAATACCTTGTGTGCTGCC 584
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; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
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; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.

APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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DB 174 TGTGCCCGCGCGGAGCAGTGACATGGGGTGTGGAGGTAGATGGGCTCCCGGCGCGGA 233
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